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December 6, 2005, 10:32:12 ; Search time 180.906 Seconds (without alignments) 686.395 Million cell updates/sec
                                                                                                                                                                                          US-10-611-655-10
944
1 MHGEGTFTSDVSSYLEGQAA......VKCEGISLLAQNTSHHHHHH 176
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                              2166443 seqs, 705528306 residues
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                            Title:
Perfect score:
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                                                                                                                 Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Minimum DB seq length: 0 Maximum DB seq length: 200000000 Database :

2166443

Total number of hits satisfying chosen parameters:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

	Description	P04216 homo sapien	pond		Q59ga0 homo sapien			P01831 mus musculu	-	gallus	gallue		ö	0	Ω	U	U	ㅁ	E	E	0	Ø			ų.		ns sndopoyd 8dn190				-	P15438 rana catesb	
	EI CI	THY1 HUMAN	OSRSOB PONPY	THY1 MACMU	QS9GAO HUMAN	Q9WUR5 CAVPO	THY1 RAT	THY1 MOUSE	Q53YX2 MOUSE	Q7T252 CHICK	THY1 CHICK	Q9XT67 CANFA	Q6PPF4 CAPHI	GLUC_SHEEP	GLUC_BOVIN	GLUC_CANFA	GLUC_CAVPO	GLUC_HUMAN	GLUC_MESAU	GLUC_MOUSE	GLUC_OCTDE	GLUC_PIG	GLUC_RAT	Q53TP6_HUMAN	Q6RYB1_9SAUR	GLUC CHICK	Q6IUP8_PHOSU	QGRYBS NEOFS	GLUC_HELSU	QGRYB6 PRODO	Q6KB05 MOUSE	GLUC_RANCA	
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*	Ouery Match	66.7	66.1	65.6		53.3	44.6	43.1	43.1	33.9	32.4	25.8	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	15.4	15.4	15.3	14.7	14.7	14.4	14	13	
	Score	630	624	619	546	503	421	406.5	406.5	320	305.5	244	157	157	157	157	157	157	157	157	157	157	157	157	145.5	145	144	139	139	136	135	125	
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Q8uwl9 hoplobatrac Q6ryb7 ictalurus p P62394 anguilla an P63295 anguilla ro P04092 lophius ame Q6rya9 sebastes ca Q4rdy tetraodon n Q6ryb2 bufo maxinu Q41143 xenopus lae Q65212 mus sp. fv/O42144 xenopus lae Q54082 xenopus lae Q54082 xenopus lae P81027 oreochromis
QBUWL9 9NEOB QGRYB7_ICTPU QGRYB7_ICTPU GLUCL_ANGAN GLUCL_ANGRO GLUC1_LOPAM QGRYA99_PERC QGRYB9_9PERC QGRYB2_BUPMA GLUC1_XENLA GLUC1_XENLA GLUC1_XENLA GLUC2_XENLA GSD082_XENLA GLUC2_CRENI
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220 120 30 30 123 123 149 266 266 219 219 33
1122.00 122.00 122.00 122.00 122.00 122.00 122.00 122.00 123.00 1
125 122 122 122 122 121 121 121 116 116
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## ALIGNMENTS

RESULT THY1 HI	THY1 HUMAN STANDARD; PRT; 161 AA.
SPE	e a
445	ದ
E E	
88	Homo sapiens (Human).
38	jora, merazoa, lia, Eutheria,
88	Homo. NCBI TaxID=9606;
Z C	[1] TOTAL SECTION SECT
ž X	
A t	Seki T., Spurr N., Obata F., Goyert S., Goodfellow P., Silver J.; "The human Thv-1 gene: structure and chromosomal location.";
굺	Proc. Natl. Acad. Sci. U.S.A. 82:6657-6661(1985).
Z 6	[2]
ž 2	NUCLECTINE SECTION S. MEDLINE=20403900; PubMed=1094468; DOI=10.1006/bbrc.2000.3282;
8	Ye Z., Connor J.R.;
R.	"cDNA cloning by amplification of circularized first strand cDNAs
R I	reveals non-IKE-regulated iron-responsive mxnas."; Biochem Biophys Res Commun 275:223-227(2000).
2 2	[3]
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
ខ្លួ	TISSUE=Amygdala;
2 5	The German consorcium; submitted (MAR-2000) to the EMRI/GenBank/DDBJ databases.
2 %	[4]
RP.	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
N X	TISSUE-Brain, and Mye; MRDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
R.	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
<b>8</b> 8	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
\$ \$	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
2	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
<b>2 2</b>	Stapleton M., Soares M.B., Bonaldo M.F., Casavant 1.D., Schetz 1.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
R.	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
2 3	Bosak S.A., McEwan P.J., McKerman K.J., Malek J.A., Gunaratne P.H.,
<b>5 5</b>	Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Æ	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
<b>a</b> a	Whiting M., Madan A., Young A.C., Shevchenko I., Boultaru G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
R R	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
æ	Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

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TISSUE=Cortex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen).
Name=THY1;
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062643;
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                       PONPY
                                                                                                                                            Pongo.
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                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 FISKYNWKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 OKVISLIACLVDOSLRLDCRHENISSSPIOYEFSLIREIKKHVLFGLYGVFEHTYRSRIN 79
                                       Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thy-1 membrane glycoprotein.
Removed in mature form.
Ig-like V-type.
GPI-anchor amidated cysteine.
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .).
N-linked (GlCNAc. .).
N-linked (GlCNAc. .).
N-linked (GlCNAc. .).
By similarity.
By similarity.
IT -> AP (in Ref. 5).
N-> H (in Ref. 1).
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0
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PROSITE; PS50815; IG. LIKE; 1.
Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein; Membrane; Signal; T-cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 630; DB 1; Length 161;
Pred. No. 2.4e-47;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2B6796DA8EE7454B CRC64;
                                                                                                                                                                                                                                                                                                                                                                membrane; TAS.
           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                             EMBL; M11749; AAA61180.1; -; Genomic_DNA.
EMBL; AR751093; AAG13904.1; -; mRNA.
EMBL; AL161958; CAB82306.1; -; mRNA.
EMBL; BC005175; AA405175.1; -; mRNA.
EMBL; BC06559; AA46559.1; -; mRNA.
EMBL; SS9749; AA826353.2; -; mRNA.
PIR; A73130; TDHI.
PIR; T47130; TAH130.
Ensembl; ENSG0000154096; Homo gapiens.
                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005887; C:integral to plasma me
GO; GO:0005886; C:plasma membrane; NAS.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-11ke.
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Best Local Similarity 99.29
Matches 121; Conservative
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H-InvDB; HIX0010195; -.
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126
130
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CARBOHYD
CARBOHYD
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QKVTSLTACLVDQSLRLDCRHENTTTSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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10-MAY-2005 (Rel. 47, Last annotation update)
Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CDw90) (CD90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta (Rhesus macaque).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                             :
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0
                                                                                                                                                                                                                                                                                       Blocker H., Society M., Bradt P., Mewes H.W., Weil B., Amid (Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CR861077; CA493158.1; -; mRNA.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
SMART; SM04406; IGV: 1.
SWART; SM04406; IGV: 1.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 161 AA; 17963 MW; 286791DDBCE0401B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.1%; Score 624; DB 2; Length 161; 97.5%; Pred. No. 8e-47; ive 3; Mismatches 0; Indels
                                   01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp459C1015.
       161 AA
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15-DEC-1998 (Rel. 37, Last seq
10-MAY-2005 (Rel. 47, Last ann
                                                                                                                                                                                                                                                                            The German cDNA Consortium;
QSR508 PONPY PRELIMINARY;
QSR508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 97.5
Matches 119; Conservative
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                                                                                                            Name=DKFZp459C1015;
                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                 NCBI_TaxID=9600;
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us-10-611-655-10.rup

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49 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKVTSLTACLVDQSLRLDCRHENTSSSPIQYBFSLTRETKGHVLFGTVGVPEHTYRSRTN 108
                36 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKGHVLFGTVGVPEHTYRSRTN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 QKVTSLTACLVNQNLALDCRHENTTTLPIQYEFSLTREKKKHVLFGTVGVPEHAYRSRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
13-ANG-1987 (Rel. 05, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CDw90) (CD90
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                        Schaefer H., Burger R., Otto A., Bartels T.;
Characterization and cloning of guinea pig Thy-1.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ238589; CA844008 1; -; mRNA.
InterPro; IPR0013599; Ig.
InterPro; IPR00110; Ig-1ike.
Fean; PP00047; ig; 1.
SMART; SM00409; IG; 1.
PP0SITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 161;
                                                             FISKYHMKVLYLSAFISKDEGTYTCALHHSGHSPPISSONVTVLR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
                                                                               PTSKYNMKVLYLSAPTSKDEGTYTCALHHSGHSPPISSQNVTVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thy-1 protein.
241461D901F80B1B CRC64;
                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.3%; Score 503; DB 2; 79.5%; Pred. No. 3.3e-36;
                                                                                                                                                                        161 AA
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                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 AA; 17995 MW;
                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen).
Name=Thy1; Synonyms=Thy-1;
                                                                                                                                                                        Q9WURS_CAVPO PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10141;
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ID _THY1_RAT
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    49
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                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISKYNMKVLYLSAFTXKDEGTYTCXLHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QKVTSLIACLVDQSLRLDCRHENTTSSPIQYEFSLTRETKGVVLFGTVGVPEHTYRSRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                   Thy-1 membrane glycoprotein.

Removed in mature form.

Ig-like V-type.

GPI-anchor amidated cysteine.

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

By similarity.

By similarity.

W, 326B135498BA401B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama
Ohara O., Nagame T., Kikuno F.R.;
"None Title.";
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                                                                                                         EMBL; U93310; AAC05640.1; -; mRNA.
InterPro; IPR00359; Ig.
Pfan; PR00047; Ig. 1.
SWART; SM00409; IG. 1.
PROSTITE; PSS0835; IG. LIKE; 1.
Membrane; Signal; T-cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.8%; Score 546; DB 2; Length 145; 99.0%; Pred. No. 4.9e-40; ive 1; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 AA; 15904 MW; 9DA4BC208DCD5766 CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Liast sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Thy-1 cell surface antigen variant (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                    uvery Match
Best Local Similarity 96.7%; Pred. No. 2.2e-46;
Matches 118; Conservative 2; Mismatchen ?
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Q59GAO;
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Matches 104; Conservative
                                                                                                                                                                                                                                                                   161
126
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TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                               161 AA;
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NUCLECTIDE SEQUENCE OF 20-161.
MEDLINE=85051865; Pubmed=6149956; DOI=10.1016/0014-5793(84)81250-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-82068190; PubMed=6118137; Campbell D.G., Gagnon J., Reid K.B.M., Williams A.F.; Campbell D.G., Gagnon J., Reid K.B.M., Williams A.F.; Mart brain Thy-1 glycoprotein. The amino acid sequence, disulphide bonds and an unusual hydrophobic region."; Biochem. J. 195:15-30(1981).
                                                                                                                                                                                                                                                                                     Moriuchi T., Chang H.-C., Denome R., Silver J.;
"Thy-1 cDNA sequence suggests a novel regulatory mechanism.";
Nature 301:80-82(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moriuchi T., Silver J.;
"Rat Thy-1 antigen has a hydrophobic segment at the carboxyl
                                                            oex1 r., Chang H.-C., Moriuchi T., Denome R., Silver J.;
"Thy-1: a hydrophobic transmembrane segment at the carboxyl
terminus.";
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SMART; SM00409; Ig. 1.
BROSITE; PRS50835; IG_LIKE; 1.
Direct protein sequencing; Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein; Membrane; Immunoglobulin acid; Sialic acid; Sialic acid; Signal; T-cell. SIGNAL
20 130 Thy-1 membrane glycoprotein.
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NUCLECTIDE SEQUENCE OF 20-161.
MEDLINE=85111162; PubMed=2857477;
Seki T., Moriuchi T., Chang H.-C., Denome R., Silver J.;
"Structural organization of the rat thy-1 gene.";
Nature 313:485-487(1985).
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Ensembl; ENSRNOG0000006604; Rattus norvegicus.
RGD; 3860; Thyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X03152; CAA26931.1; -; Genomic_DNA.
EMBL; X03150; CAA2693.1; -; mENA.
EMBL; X02002; CAA26033.1; -; GENOMIC_DNA.
EMBL; M18002; AAA4243.1; -; mENA.
EMBL; M10666; AAA42242.1; -; mENA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0009986; C:cell surface; TAS
                                                      MEDLINE=86005549; PubMed=2864289;
                                                                                                                                                                                                                                                         MEDLINE=83115223; PubMed=6130472;
                                                                                                                                                                  Fed. Proc. 44:2865-2869(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 178:105-108(1984).
                                                                                                                                                                                                      [2]
NUCLEOTIDE SEQUENCE OF 1-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN SEQUENCE OF 20-130
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                           NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 LFSDRPIKVLTLANFTTKDEGDYMCELRVSGQNPTSSNKTINVIRDKLVKCGGISLLVQN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 QRVISLTACLVNQNLRLDCRHENNTNLPIQHEFSLTREKKKHVLSGTLGVPEHTYRSRVN 79
                    Ig-like V-type.

Pyrrolidone carboxylic acid.

Pyrrolidone carboxylic acid.

Relinked (GlcNAc. .) (high mannose or complex); in thymus.

N-linked (GlcNAc. .) (high mannose); in brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OKVTSLTACLVDOSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostoml,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=85115360; PubMed=2857501;
Seki T., Chang H.-C., Moriuchi T., Denome R., Ploegh H., Silver J.;
"A hydrophobic transmembrane segment at the carboxyl terminus of thy-
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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10-MAY-2005 (Rel. 47, Last annotation update)
Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CDw90) (CD90
                                                                                                                                                                                                                                       . .) (high mannose
                                                                                                                                                                                             (complex); in
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                                                                                                                                                                                                                                                                                                                                                                                        44.6%; Score 421; DB 1; Length 161; 67.2%; Pred. No. 5.1e-29; ive 15; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                             71 71 B -> Q (in Ref. 1).
161 AA; 18172 MW; 3285748F3C2C5AB2 CRC64;
                                                                                                                                                                      (GlcNAc. . .)
Removed in mature form.
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Chang H.-C., Sekf.T., Moriuchi T., Silver J.;
"Isolation and characterization of mouse Thy-1 g
Proc. Natl. Acad. Sci. U.S.A. 82:3819-3823(1985)
                                                                                                                                                                                                                                     N-linked (GlcNAc. hybrid); in brain.
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NUCLECTIDE SEQUENCE (THY-1.2 ALLOTYPE).
MEDLINE=86113437; PubMed=2868059;
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MEDLINE=86055760; PubMed=2866091;
MEDLINE=86055760; R.-I., Grosveld F.;
"Structure of the murine Thy-1 gene.";
                                                                                                                                                                        N-linked
N-linked
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                                                                                                                                                                                                                     thymus
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21-JUL-1986 (Rel. 01, Last seq
10-MAY-2005 (Rel. 47, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Thyl; Synonyms=Thy-1;
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 227:649-651(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                       82; Conservative
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161
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P01831;
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STRAIN-FVB;
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DISULFID
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Best Local
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Q7T252_CHICK
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XX Staueberg R.L., Ferigold B.A., Grouse L.H., Derge J.G.,

A Straueberg R.L., Ferigold B.A., Grouse L.H., Derge J.G.,

X Klaueberg R.L., Ferigold B.A., Grouse L.H., Derge J.G.,

X Klauener R.D., Collins F.S., Warger L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A platchenk C.L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

N Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Perers G.J., Abrameon R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Halton M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                   "The mouse Thy-1.2 glycoprotein gene: complete sequence and identification of an unusual promoter."; J. Immunol. 136:1482-1489(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ensembl; ENSMUSGG0000032011; Mus musculus.
MGI; MGI:98747; Thy1.
GO; GO:0009897; C:sernal side of plasma membrane; IDA.
InterPro: IPROG110; Ig-11ke.
PROSITE; PS50835; IG_LIXE; 1.
Direct protein sequencing; Glycoprotein; GPI-anchor;
Immunoglobulin domain; Lipoprotein; Membrane; Polymorphism;
Pyrrolidone aboxylic acid; Signal; T-ceili.
SIGNAL
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Removed in mature form.
Ig-like V-type.
Pyrrolidone carboxylic acid.
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N-linked (GlCNAc. . .).
N-linked (GlCNAc. . .).
                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X03151; CAA26930.1; -; Genomic_DNA.

EMBL; X02771; CAA26548.1; -; Genomic_DNA.

EMBL; X02772; CAA26549.1; ALT SEQ; Genomic_DNA.

EMBL; X02774; CAA26550.1; ALT SEQ; Genomic_DNA.

EMBL; M10246; AAA40440.1; -; Genomic_DNA.

EMBL; M1160; AAA40441.1; -; Genomic_DNA.

EMBL; M12779; AAA40441.1; -; Genomic_DNA.
                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC054436; AAH54436.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131
162
127
20
131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X02773;
EMBL; M10246;
EMBL; M11160;
EMBL; M12379;
EMBL; BC05443(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 NFTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSONVTVLRDKLVKCEGISLLAQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 TISNQPYIKVITLANFTTKDEGDYFCELRVSGANPMSSNKSISVYRDKLVKCGGISLLVQ 139
                                                                                                                                                                                                                                                                                                              108 NPTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 QKVTSLTACLVNQNLRLDCRHENNTKONSIQHEFSLTREKRKHVLSGTLGIPEHTYRSRV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delaitre E., Jean L., Tron F., Boyer O.;
A single amino acid substitution confers CD90.1 (Thyl.1) allotype specificity.",
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.1%; Score 406.5; DB 2; Length 162; 65.0%; Pred. No. 9.7e-28; Indels 1; ive 20; Mismatches 22; Indels 1;
                                                                                                                 ; Score 406.5; DB 1; Length 162; ; Pred. No. 9.7e-28; 20; Mismatches 22; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AX445633, AAR17087.1; -; mRNA.
Ensembl; ENSMUSG0000032011; Mus musculus.
MG1:90747; Thy1.
GQ; GO:0009997; C:external side of plasma membrane; IDA.
InterPro; IPR00710; Ig-11ke.
InterPro; IPR003596; Ig-v.
SWART; SM00406; IGv; 1.
FROSTE; PS06035; IG_LKE; 1.
Immunoglobulin domain.
SEQUENCE 162 AA; 18108 MW; 6978F4D3A9F2C530 CRC64;
                                               108 Q -> R (in allele Thy-1.1).
18080 WW; 397BF7D3A9F2C77B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 AA
                                                                                                                        43.1%;
                                                                                                                                          l Similarity 65.04
80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QS3YX2_MOUSE PRELIMINARY;
QS3YX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
28 1
38 1
108 1
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TS 170
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                                                                                        domain.
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                                                                                                                                                                                                                                                                                                                                                                                49 OKVISLIACIVDOSLRIDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
                                                                                                                                                                                                                                                                                                                                                                                                                           109 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
                                                                                                                                                                                                                                                                                                                                                                                            20 QMIRDLSACLLGQSLRVDCRYENKTSDPLTYFFSLTKDNRKHIIQSTISVSENVYRNRAN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 43-55; 59-79 AND 81-101.
                                                                                                                                         NUCLEOTIDE SEQUENCE.
PubMed=14711516; DOI=10.1016/j.pep.2003.10.011;
Mehndiratta P., Walton W.J., Hare J.T., Pulido S., Parthasarathy G., Emmett M.R., Marehall A.G., Logan T.M.;
"Expression, purification, and characterization of avian Thy-1 from Lec! nammalian and Th5 insect cells.";
Protein Expr. Purif. 33:274-287(2004).
EMBL; AY230132; AAP31241.1; -; MRNA.
Ensembl; ENSCALGO000006751; Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=White leghorn; TISSUE=Brain; MEDL:1016/0169-328X(92)90180-J; MEDL:NE=393601794; WDMed=135971; DOI=10.1016/0169-328X(92)90180-J; DOWSING B.U.; Gooley A.A.; Gunning P., Cunningham A., Jeffrey P.L.; Molecular cloning and primary structure of the avian Thy-1
                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                   33.9%; Score 320; DB 2; Length 160; 48.4%; Pred. No. 3.7e-20;
                                                                                                                                                                                                                                                                                                                                                          39; Indels
                                                                                                                                                                                                                                                                                                              160 AA; 18061 MW; 6DC39D8519540CE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Thy-1 membrane glycoprotein precursor (Thy-1 antigen).
                                Last sequence update)
Last annotation update)
160 AA
                                                                                                                                                                                                                                                                                                                                                         59; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 AA
                     Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                           SMART, SM00409, ĬG; 1.
PROSITE, PS50835, IG LIKE; 1.
Immunoglobulin domain.
                                                                                                                                                                                                                                             InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                   01-OCT-2003 (TrEMBLrel 25, 01-OCT-2003 (TrEMBLrel 25, 01-MAR-2004 (TrEMBLrel 26,
                                                                                                                                                                                                                                                                                                                                                48.48;
Q7T252 CHICK PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                  Pfam; PF00047; ig;
                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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                                                               Name=THY1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=THY1;
                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                     Query Match
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This Swiss-Frot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMHL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QMIRDLSACLLGGSLRVDCRYENKTSNPLTYEFSLTRQ-QKHIIQSTISVSENVYRNRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN
TISSUE SPECIFICITY: Forebrain, cerebellum and tectum.

DEVELOUPENTAL STAGE: It is detected at embryonic day 4 (E4) in forebrain and tectum. There is an increase in levels between E16 and the first few days post-hatch. During E19 to hatch a rapid reduction in the levels is seen with a general increase in expression in adulthood.

FIN: The N. terminus is blocked.

SIMILARITY: Contains 1 19-like V-type (immunoglobulin-like)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.9e-19;
ches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 48.4%; Pred. No. 6.9e tes 59; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 305.5;
Pred. No. 6.9
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                                                                                                                                                                                                                                                                                                                              EMBL; S47368; AAA11889.1; -; mRNA.
EMBL; L14924; AAC42216.1; -; mRNA.
PIR; A48975; A48975.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSXT67_CANFA PRELIMINARY;
Q9XT67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thy-1 (Fragment).
Name=Thy1;
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EMBL; AF529185; AAM94409.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
                                                                             NCBI_TaxID=9940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity
                             Name=GCG
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10-MAX-2005 (Rel. 47, Last annotation update)
Glucagon precursor [Contains: Glicentin, Glicentin-related polypeptide (GRPP); Oxyntomodulin (OXY) (OXM); Glucagon; Glucagon-like peptide 1
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Caprinae, Capra.
         NUCLECTIDE SEQUENCE.

MEDLINES-92656967; PubMed=10331940; DOI=10.1006/geno.1999.5772;

Li R., Mignot B., Paraco J., Kadotani H., Cantanese J., Zhao B.,

Lin X., Hinton L., Ostrander E.A., Patterson D.F., de Jong P.J.;

"Construction and characterization of an eightfold redundant dog
genomic bacterial arrificial chromosome library.";
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                                                                                                                                                                                                                                                                                                                                                                                                                           Ballester M., Castello A., Ibanez E., Sanchez A., Folch J.M.; Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS88290; AAT00451.1; -, Genomic_DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005179; F:hormone activity; IEA.
                                                                                                                                                                                Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                Kodatani H., Mignot E.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF103747; AAD40573.1; -; Genomic DNA.
Ensembl; ENSCAFG00000012021; Canis famīliaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B538A926E9447F80 CRC64;
                                                                                                                                                            60 AA; 6700 MW; 97AFAD948FD8D054 CRC64;
                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                               Score 244; DB 2; L. Pred. No. 5.3e-14; 5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 157; DB 2;
Pred. No. 1.6e-06;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                            45 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGEGTFTSDVSSYLEGOAAKEFIAWLVKGRG 32
                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 45, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000532; Glucagon.
                                                                                                                                                                              25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 AA; 5179 MW;
                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.6%;
96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00123; Hormone 2; 1.
PRINTS; PR00275; GLUCAGON.
SMART; SM00070; GLUCA; 1.
                                                                                                                                                                                                                                                                                           QEPPF4 CAPHI PRELIMINARY;
QEPPF4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 96.8°
Matches 30; Conservative
                                                                                                                                                                                         Local Similarity 78.3
Les 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                          Glucagon (Fragment)
Capra hircus (Goat)
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9925;
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Q8MJZ5;
25-OCT-2004
25-OCT-2004
10-MAY-2005
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Submitted Voll-2007, to the Embal/Calabank/Dub untabases.
-!- FUNCTION: Glucagon plays a key role in glucose metabolism and homeostasis. Regulates blood glucose by increasing gluconeogenesis and decreasing glycolysis. A counterregulatory hormone of insulin, raises plasma glucose levels in response to insulin-induced hypoglycemia (By similarity).
-!- FUNCTION: GLP-1 is a potent stimulator of glucose-dependent insulin release. Play important roles on gastric motility and the suppression of plasma glucogon levels. May be involved in the suppression of plasma glucogon levels. May be involved in the suppression of satiety and stimulation of glucose disposal in peripheral tissues, independent of the actions of insulin. Have growth-promoting activities on intestinal epithelium. May also regulate the hypothalamic pltuitary axis (HPA) via effects on LH, TSH, GRH, oxytocin, and vasopressin (By similarity).
-!- FUNCTION: GLP-2 stimulates intestinal growth and up-regulates villus height in the small intestine, concomitant with increased crypt cell proliferation and decreased enterocyte apoptosis. The gastrointestinal tract, from the stomach to the colon is the principal target for GLP-2 action. Plays a key role in nutrient homeostasis, enhancing nutrient assimilation through enhanced gastrointestinal function, as well as increasing nutrient disposal. Stimulates intestinal glucose transport and decreases mucosal permeability (By similarity).
-!- FUNCTION: Oxyntomodulin significantly reduces food intake (By et al. 2014)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIMILERILY).

1- FUNCTION: Glicentin may modulate gastric acid secretion and gastro-pyloro-duodenal activity.

1- SUBCELLULAR LOCATION: Secreted.

1- SUBCELLULAR LOCATION: Secreted.

1- TISSUB SPECIFICITY: Glucagon is secreted in the A cells of the islets of Langerhans. GLP-1, GLP-2, oxyntomodulin and glicentin are secreted from entercendocrine cells throughout the gastrointestinal tract. GLP1 and GLP2 are also secreted in selected neurons in the brain.

1- INDUCTION: Glucagon release is stimulated by hypoglycemia and inhibited by hyperglycemia, insulin, and somatostatin. GLP-1 and GLP-2 are induced in response to nutrient ingestion (By
(GLP-1); Glucagon-like peptide 1(7-37) (GLP-1(7-37)); Glucagon-like peptide 1(7-36) (GLP-1(7-36)); Glucagon-like peptide 2 (GLP-2)]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Limesand S.W., Hay W.W. Jr.; "Characterization of the endocrine pancreas in an ovine placental insufficiency IUGR fetus."; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               Ovis ariės (Sheep).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                            Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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NUCLEOTIDE SEQUENCE.
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Drucker D.J.
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Glucagon-like peptide 1(7-36) (By
similarity).
By similarity).
Glucagon-like peptide 2 (By similarity).
Cleavage (by PCSK2) (By similarity).
Cleavage (by PCSK1 and PCSK2) (By
similarity).
Cleavage (by PCSK1) (By similarity).
Cleavage (by PCSK1) (By similarity).
Cleavage (by PCSK1) (By similarity).
Cleavage (by PCSK1) (By similarity).
Cleavage (by PCSK1) (By similarity).
Cleavage (by PCSK1) (By similarity).
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                                                                                                                                                                                                                                                                                                                  By similarity.
Glucagon-like peptide 1 (By similarity).
Glucagon-like peptide 1(7-37) (By
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Lopez L.C., Frazier M.L., Su C.-J., Kumar A., Saunders G.F.;
"Mammallan pancreatic preproglucagon contains three glucagon-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amide (G-128 provides amide
                                                                                                                         basic residues; Glucagon family;
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                                                                                                                                                                                             Glicentin (By similarity).
Glicentin-related polypeptide (By
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MEDLINE=71166445; PubMed=5102927;
Bromer W., Boucher M.E., Koffenberger J.E. Jr.;
"Amino acid sequence of bovine glucagon.";
J. Biol. Chem. 246:2822-2827(1971).
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Pred. No. 8.2e-06;
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(Rel. 05, Last sequence update)
(Rel. 48, Last annotation update)
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InterPro; IPR000532; Glucagon.
Pfam; PR00123; Hormone 2; 3.
PRINTS; PR00275; GLUCAGON.
SMATT; SM00070; GLUCA; 3.
PROSITE; PS00260; GLUCAGON; 4.
Amidation; Cleavage on pair of b
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ilarity 96.8%;
Conservative
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Best Local Similarity
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13-AUG-1987 (
13-SEP-2005 (
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P01272;
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MEDILINE-22446611; PubMed=1255744; DOI=10.1210/me.2000-0306; RT Gituagano-like peptidae: regulators of cell proliferation, differentiation, and apoptosis.; A differentiation, and apoptosis.; A differentiation, and apoptosis.; RE MEDILINE-222109; PubMed=12626323; DOI=10.1157/ajpendo.00492.2002; RE MEDILINE-222109; PubMed=12626323; DOI=10.1157/ajpendo.00492.2002; Jang B. B., Gardenthol. 244.8671.8678(2003). Land G. Sand B. B., Gardenthol. 244.8671.8678(2003). Land G. Sand B. B., Gardenthol. 244.8671.8678(2003). Land G. Sand G. San
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NCBI_TaxID=9615;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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P29794; Q95LG0;
01-APR-1993 (Rel. 25, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Glucagon precursor [Contains: Glicentin, Glicentin-related polypeptide (GRPP); Oxyntomodulin (OXY) (OXM); Glucagon; Glucagon-like peptide 1 (GLP-1); Glucagon-like peptide 1 (GLP-1); Glucagon-like peptide 2 (GLP-1); Glucagon-like peptide 2 (GLP-2)); Glucagon-like
                                                                                                                                                                                                                                    similarity).
Oxyntomodulin (By similarity).
Glucagon.
By similarity.
Glucagon-like peptide 1 (By similarity).
Glucagon-like peptide 1(7-37) (By
 further N-terminally truncated by posttranslational processing in the intestinal L cells resulting in GLP-1(7-3f) GLP-1-(7-36) amide. The C-terminal amidation is neither important for the metabolism of GLP-1 nor for its effects on the endocrine pancreas (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GapB
                                                                                                                                                                                                                                                                                                                                    peptide 2 (By similarity)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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(By similarity).
(By similarity).
(By similarity).
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Cleavage (by PCSK1 and PCSK2) (By
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                                                                                                                                                                PRINTS; PRO0275; GLUCAGON.
PROSTIE; PS00260; GLUCAGON.
3D-structure; Amidation; Cleavage on pair of basic residues;
Direct procein sequencing; Glucagon family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 157; DB 1; Length 180;
Pred. No. 8.4e-06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                Glicentin (By similarity). Glicentin-related polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20944 MW; 8D9B4FF05B9F15FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             group) (By similarity).
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PCSK1)
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                                      similarity).
SIMILARITY: Belongs to the glucagon family.
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Cleavage (by PCS
Cleavage (by PCS
Cleavage (by PCS
Cleavage (by PCS
Arginine amide (
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                                                                                                                                                                                                                                                                                                                   similarity).
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                                                                                                                           EMBL; K00107; AAA30538.1; -; mRNA.
                                                                                                                                     PDB; 1KK6; NMR; A=53-81.
InterPro; IPR000532; Glucagon.
Pfam; PF00123; Hormone_2; 3.
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illarity 96.8%;
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Rieffer T.J., Habener J.P.;

Kieffer T.J., Habener J.P.;

The glucagon-like peptides.";

Endocr. Rev. 20:876-913(1999).

The glucagon-like peptides.";

Endocr. Rev. 20:876-913(1999).

I Endocr. Rev. 20:876-913(199).

I Endocr. Rev. 20:876-913(1
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Damholt A.B., Buchan A.M., Holst J.J., Kofod H.;
Proglucagon processing profile in canine L cells expressing
Proglucagon probramene convertase 1/3 and prohormone convertase 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89185675; PubMed=3238052; DOI=10.1016/0167-0115(88)90230-3;
                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shinomura Y., Eng J., Yalow R.S.; "Immunoreactive glucagons purified from dog pancreas, stomach and
                                                                                                                                        Irwin D.M.; "cDNA cloning of proglucagon from the stomach and pancreas of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drucker D.J.; "Glucagon-like peptides: regulators of cell proliferation, differentiation, and apoptosis."; Mol. Endocrinol. 17:161-171(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jiang G., Zhang B.B.; "Glucagon and regulation of glucose metabolism."; Am. J. Physiol. 284:E671-E678(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=12626323; DOI=10.1152/ajpendo.00492.2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drucker D.J.;
"Glucagon-like peptide 2.";
Trends Endocrinol. Metab. 10:153-156(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=12554744; DOI=10.1210/me.2002-0306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrinology 140:4800-4808(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Regul. Pept. 23:299-308(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROCESSING BY PCSK1 AND PCSK2
                                          IISSUE=Pancreas, and Stomach;
PubMed=11916259;
                                                                                                                                                                                                                                                                                       DNA Seq. 12:253-260(2001).
                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 21-89.
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10322410;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                      PTM: Proglucagon is posttranslationally processed in a tissue-specific manner in pancreatic A cells and intestinal L cells. In gancreatic A cells, the major bioactive hormone is glucagon cleaved by PCSK2/PC2. In the intestinal L cells PCSK1/PC1 liberates GLP-1, GLP-2, glicentin and oxyntomodulin. GLP-1 is further N-terminally truncated by posttranslational processing in the intestinal L cells resulting in GLP-1(7-37) GLP-1-756) amide. The C-terminal amidation is neither important for the metabolism of GLP-1 nor for its effects on the endocrine pancreas (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide 2 (By similarity).
                                                                                                                                                                                     INDUCTION: Glucagon release is stimulated by hypoglycemia and inhibited by hyperglycemia, insulin, and somatostatin. GLP-1 and GLP-2 are induced in response to nutrient ingestion (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxyntcomodulin (By similarity).

Glucagon (By similarity).

By similarity.

Glucagon-like peptide 1.

Glucagon-like peptide 1(7-37).

Glucagon-like peptide 1(7-36).

By similarity.

Glucagon-like peptide 2 (By similarity).

Cleavage (by PCSK1).

Arginina amide (G-128 provides amide group) (By similarity).
                                            -!- FUNCTION: 3/dicentin may modulate gastric acid secretion and gastro-pyloro-duodenal activity.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Glucagon is secreted in the A cells of the islets of Langerhans. GLP-1, GLP-2, oxyntomodulin and glicentin are secreted from entercondocrine cells throughout the gastrointestinal tract. GLP1 and GLP2 are also secreted in selected neurons in the brain.
mucosal permeability (By similarity).
FUNCTION: Oxyntomodulin significantly reduces food intake (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glicentin-related polypeptide (By similarity);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct protein sequencing; Glucagon family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the glucagon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01274; IGCN.
Ensembl; ENSCAFO0000100141; Canis familiaris.
InterPro; IPR00053; Glucagon.
PRINTS; PR00275; GLUCAGON.
SMART; SM00070; GLUCA, 3.
PRINTS; SR00270; GLUCA, 3.
Amidation; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glicentin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF308439; AAL09425.1; -; mRNA.
PIR; A60318; GCDG69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21115 MW;
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Gaps

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Query Match
16.6%; Score 157; DB 1; Length 180;
Best Local Similarity 96.8%; Pred. No. 8.4e-06;
Matches 30; Conservative 0; Mismatches 1; Indels

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Search completed: December 6, 2005, 10:41:51 Job time : 181.906 secs Н

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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December 6, 2005, 10:32:12; Search time 29.4355 Seconds (without alignments) 575.296 Million cell updates/sec Run on:

US-10-611-655-10 944 1 MHGEGTFTSDVSSYLEGQAA......VKCEGISLLAQNTSHHHHHH 176 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Thy-1 membrane gly	thy-1 membrane gly	Thy-1 membrane gly	Thy-1 glycoprotein								glucagon precursor	glucagon precursor	proglucagon - chic	Ig heavy chain V r	glucagon precursor	glucagon-like pept	glucagon-like pept	N					Brn-3.2 - mouse	gene Brn-3b protei	glucagon precursor	glucagon II precur	glucagon-like pept
SUMMAKIES	ΙD	TDHU	TDRT	TDMS	A48975	GCPG	GCBO	GCHY	GCGP	GCHU	GCRT	GCRTDU	A57294	GCCH	151301	A56446	GCFGB	C61125	B61125	GCAF2	151093	151058	GCIDC	GCGXA	158156	138502	GCONC	151057	S44473
	80		٠,	Н	N	-	Н	ч	Н	Н	-	Н	~	-	N	~	-	~	~	-1	N	N	Н	Н	~	~	Н	N	~
	Query Match Length	161	161	162	160	158	180	180	180	180	180	180	180	151	206	268	101	30	30	122	99	178	63	72	411	410	9	178	30
٠	Query Match	67.5	44.6	43.1	32.4	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	15.4	15.4	13.5	13.2	12.9	12.9	12.9	12.1	12.1	12.0	11.9	11.9	11.6	11.5	11.5	11.3
	Score	637	421	406.5	305.5	157	157	157	157	157	157	157	157	145	145	127	125	122	122	122	114	114	113	112	112	109.5	109	109	107
	Result No.	<b>н</b> с	<b>1</b> m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

exendin-4 - Gila m qlucaqon precursor	alpha-fetoprotein	glucagon i precurs glucagon - marbled	developmental prot	glucagon G2 - Nort hypothetical prote	protein F53C3.6 [i	glucagon - smaller	glucagon G1 - Nort	GCR 101 protein -	single chain Fv an	glucagon - elephan	fork head domain p	AF17 protein - hum
HWGH4G GCFIS	A41948	GCAF S07211	T17406	S44472 T43449	H88114	GCDF	S44471	849193	841374	GCEN	859870	138533
	н.	H (7	01	N N	0	Н	N	N	N	н	N	~
39	2783	124 29	1022	31	160	59	31	239	249	29	208	1093
10.5	10.4	10.2	10.1	10.1	10.0	10.0	6.6	9.6	9.8	9.7	7.6	9.7
39.5	98.5	96.5 96	95.5	92	94.5	94	93	92.5	92.5	92	92	92
30	35	3 3 4 3	35	36	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1
_	THOL
	Iny-1 membrane giycoprotein precursor - muman
	N'Alternate names: Thy-1 antigen
	C;Species: Homo sapiens (man)
_	C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Ju1-2004
	C;Accession: A02106
	R;Seki, T.; Spurr, N.; Obata, F.; Goyert, S.; Goodfellow, P.; Silver, J.
	Proc. Natl. Acad. Sci. U.S.A. 82, 6657-6661, 1985
	A;Title: The human Thy-1 gene: structure and chromosomal location.
	A;Reference number: A02106; MUID:86016759; PMID:2864690
	A;Accession: A02106
_	A;Molecule type: DNA
	A;Residues: 1-161 <sek></sek>
	A; Cross-references: UNIPROT: P04216; UNIPARC: UP10000049811; GB:M11749; NID: 9339682; PIDN
	C;Genetics:
	A;Gene: GDB:THY1
	A;Cross-references: GDB:119614; OMIM:188230
-	A;Map position: 11q22.3-11q23
	A;Introns: 13/1; 125/1
	C; Superfamily: immunoglobulin V region; immunoglobulin homology
	C;Keywords: glycoprotein; thymocyte; transmembrane protein
	P;1-19/Domain: signal sequence #status predicted <sig></sig>
	F;20-161/Product: Thy-1 membrane glycoprotein #status predicted <mat></mat>
_	F;20-141/Domain: extracellular #status predicted <bxl></bxl>
	F;31-106/Domain: immunoglobulin homology < IMM>
	F;142-161/Domain: transmembrane #status predicted <tmm></tmm>
	F;42,119,139/Binding site: carbohydrate (Asn) (covalent) #status predicted
	Query Match 67.5%; Score 637; DB 1; Length 161;
	Similarity 100.0%;
	יייים ווייים מיייים
	Qy 49 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
	Db 20 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 79
	QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
	DD 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139
	Ov 169 TS 170
	Db 140 TS 141

RESULT 2
147130
hypothetical protein DKFZp761B15121.1 - human
hypothetical protein DKFZp761B15121.1 - human
C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47130

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8 셤 셤 δ 셤

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A; Molecule type: mRNA
A; Residues: 1-122 < MO2.
A; Residues: 1-122 < MO2.
A; Cross-references: UNIPARC; UPI0000173744
C; Comment: This glycoprotein is a major constituent of brain-cell membrane and is abunda
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin V region; pyroglutamic acid
F; 1-19/Domain: signal sequence #status predicted < SIG>
F; 20-130/Product: thy.1 membrane glycoprotein #status experimental < MAT>
F; 21-106/Domain: immunoglobulin homology < IMM>
F; 20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer
F; 28-130, 38-104/Disulfide bonds: #status experimental
F; 28-130, 3117/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A,Resdudes: 1-162 <58K.>

A,Resdudes: 1-162 <58K.>

A,Cross-references: UNIPROT:P01831; UNIPARC:UPI000002395E; GB:M10246; NID:g202032; PIDN:

B,Giguere, V.; Isobe, K.I.; Grosveld, F.

EMBO J. 4, 2017-2024, 1985

A,Title: Structure of the murine Thy-1 gene.

A,Reference number: A24647; MUID:86055760; PMID:2866091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thy-1 membrane glycoprotein precursor - mouse C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Decies: Mus musculus (house revision 28-May-1986 #text change 09-Jul-2004 C;Decession: A94278; A24647; A94265; IS9028; IS5957; A02I08 R;Seki, T.; Chang, H.C.; Morluchi, T.; Denome, R.; Ploegh, H.; Silver, J. Science 227, 469-651, 1985 Science 227, 469-651, 1985 A;Title: A hydrophobic transmembrane segment at the carboxyl terminus of Thy-1. A;Reference number: A94278; MUID:85115360; PMID:2857501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 LFSDRFIKVLTLANFTTKDEGDYMCELRVSGQNFTSSNKTINVIRDKLVKCGGISLLVQN 139
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A;Title: Neuronal cell Thy-1 glycoprotein: homology with immunoglobulin. A;Reference number: A94265; MUID:82199396; PMID:6177036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: A94265
A,Molecule type: protein
A,Residues: 20-131 <MIL>
A,Cross-references: UNIPARC:UP10000173745
A,Note: the Thy-1.1 sequence differs from that shown in having 108-Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
    A; Molecule type: protein
A; Residues: 20-130 <CAM>
A; Cross: 20-130 <CAM>
A; Cross: Loterences: UNIPARC: UPI0000173743
A; Note: this sequence shows homologies with immunoglobulin domains
R; Morluchi, T.; Chang, H.C.; Denome, R.; Silver, J.
Nature 301, 80-82, 1983
A; Title: Thy-1 cDNA sequence suggests a novel regulatory mechanism.
A; Reference number: A93296; MUID: 83115223; PMID: 6130472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 44.6%; Score 421; DB 1; Length 161; Best Local Similarity 67.2%; Pred. No. 1.9e-29; Matches 82; Conservative 15; Mismatches 25; Indels
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A,Experimental source: strain BALB/c
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A; Residues: 1-162 <GIG>
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thy. Imembrane glycoprotein precursor - rat

thy. Imembrane glycoprotein precursor - rat

Nathernae names (thy. antigan

C. Adcession: B45509; A45509; A25555; A21652, A30311; A3256; A02107

R. Sekk, T. Workuchi, T.; Chang, H.C.; Denome, R.; Silver, G.

A. Accession: B45509; A45509; MUDD:B5111162; PMID:2857477

A. Accession: B45509; MUDD:B5111162; PMID:2857477

A. Accession: A45509

A. Accession: B45509; MUDD:B5111162; PMID:2857477

A. Accession: A45509

A. Accession: A45009

A. 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 FISKYNMKVLYLSAFISKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                          A,Accession: T47130
A/Status: preliminary
A/Status: mRNA
A,Molecule type: mRNA
A,Residuss: 1-161 <AAA>
A,Cross-references: UNIPROT:P04216, UNIPARC:UP10000136F1F; EMBL:AL161958
A,Experimental source: adult amygdala; clone DKFZp761B15121
C,Genetics: A,Note: DKFZp761B15121.1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, S. submitted to the Protein Sequence Database, March 2000 A;Reference number: 224374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.7%; Score 630; DB 2; Length 16 Best Local Similarity 99.2%; Pred. No. 1.5e-47; Matches 121; Conservative 1; Mismatches 0; Indels
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A,Cross-references: UNIPARC:UP1000002C9AC
A,Note: this peptide is co-secreted with glucagon from the pancreas
R,Bromer, W.W.; Sinn, L.G.; Behrens, O.K.
A,Am. Chem. Soc. 79, 2807-2810, 1957
A,Title: The amino acid sequence of glucagon. V. Location of amide groups, acid degrada.
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R;Orskov, C.; Bersani, M.; Johnsen, A.H.; Hojrup, P.; Holst, J.J.
Chim. 264, 12826-12829, 1989
A;Title: Complete sequences of glucagon-like peptide-1 from human and pig small intesti.
A;Reference number: A92732; MUID:89327238; PMID:2753890
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A; Residues: 111-158 (20H).
A; Residues: 111-158 (20H).
A; Residues: 111-158 (20H).
A; Residues: 111-158 (20H).
C; Comment: K's represent missing amino acids, mostly basic, that are predicted to exist C; Comment: K's represent missing amino acids, mostly basic, that are predicted to exist C; Superfamily: glucagon
C; Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; intes F; 1-1-30/Region: glucagon-69 #status experimental cg69.
F; 1-30/Region: glucagon-37 #status predicted cd37.
F; 33-61/Product: glucagon-1ike peptide 1 #status experimental cGii.>
F; 78-107/Product: glucagon-like peptide 2 #status experimental cGii.>
F; 126-158/Product: glucagon-like peptide 2 #status experimental cGii.>
F; 126-158/Product: glucagon-like peptide 2 #status experimental cGii.>
F; 126-158/Product: glucagon-like peptide 2 #status experimental cGii.>
F; 107/Modified site: amidated carboxyl end (Arg) (amide in mature form from following g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucagon precursor - pig (fragment)
N;Alternate names: glicentin; oxyntomodulin
N;Contains: glicentin-related poptide; glucagon; glucagon-37 (oxyntomodulin); glucagon-70; oxyntomodulin); glucagon-70; oxyntomodulin, glucagon-70; oxynt
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R;Buhl, T.; Thim, L.; Kofod, H.; Orskov, C.; Harling, H.; Holst, J.J.
Sbol. Chem. 263, 8621-8624, 1988
A;Title: Naturally occurring products of proglucagon 111-160 in the porcine and A;Reference number: A28064; MUID:88243712; PMID:3379036
                                                                                                                                                                                               99 VTWHKNLVCLYLHSFTTSDEGVYMCELKATNDYTGNQIKNITVIKDKLEKCVRLSLLIQN 138
                  20 QMIRDLSACLLGQSLRVDCRYENKTSNPLTYEFSLTRQ-QKHIIQSTISVSENVYRNRAN 78
                                                                                                                                        109 FISKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN
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A;Regidues: 1-69 <TH1>
A;Cross-references: UNIPARC:UPI0000173500
R;Thin, L.; Moody, A.J.
Regul. Pept. Suppl. 2, S33, 1983
A;Title: Primary structure of a possible porcine proglucagon fragment.
A;Reference number: A60312
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Regul. Pept. 2, 139-150, 1981
Arjtile: The primary structure of porcine glicentin (proglucagon). A;Reference number: A94233; MUID:81248172; PMID:6894800
A;Accession: A01540
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A,Molecule type: protein
A,Residues: 33-61 <BRO>
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C; Superfamily: immunoglobulin V region; immunoglobulin nomology
C; Seyvords: glycoprotein; pyroglutemic acid; T-cell; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-162/Product: Thy-1 membrane glycoprotein #status predicted <MAT>
F;31-10/Domain: immunoglobulin homology <IPM>
F;31-10/Domain: immunoglobulin homology <IPM>
F;43-162/Domain: transmembrane #status predicted <TPM>
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment F;20/Modified site: carbohydrate (Asn) (covalent) #status experimental
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: UNA
A;Molecule type: DNA
A;Molecule type: UNIPARC:UPI000002395B; GB:M12379; NID:g202040; PIDN:AAA40443.1; PID:
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AjRossarveerences: UNTPARC:UPI000002395E; GB:M11160; NID:g202034; PIDN:AAA40441.1; PID: Ajrossarveerences: UNTPARC:UPI000002395E; GB:M1160; NID:g202034; PIDN:AAA40441.1; PID: R; Ingraham, H.A.; LawlesB, G.M.; Bvans, G.A.
J. Immunol. 136, 1482-1489, 1986
Ajrille: The mouse Thy-1.2 glycoprotein gene: Complete sequence and identification of an Ajrille: The mouser: 155957; MUID:86113437; PMID:2868059
Ajrocession: 155957
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R;Dowsing, B.J.; Gooley, A.A.; Gunning, P.; Cunningham, A.; Jeffrey, P.L.
R;Dowsing, B.J.; Gooley, A.A.; Gunning, P.; Cunningham, A.; Jeffrey, P.L.
Brain Res. Mol. Brain Res. 14, 250-260, 1992
A;Title: Molecular cloning and primary structure of the avian Thy-1 glycoprotein.
A;Reference number: A48975; MUID:93061794; PMID:1359371
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C;Species: Gallus gallus (chicken)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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A;Map position: 9
A;Introns: 13/1; 126/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin pyroglutamic acid; T-cell; transmembration of the control of 
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Proc. Natl. Acad. Sci. U.S.A. 82, 3819-3823, 1985
A;Title: Isolation and characterization of mouse Thy-1
A;Reference number: IS9028; MUID:85216583; PMID:2582427
A;Accession: IS9028
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48.4%; Pred. No. 1.9e-19;
tive 25; Mismatches 37
                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Best Local Similarity 48.4%
Matches 59; Conservative
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Best Local Similarity 65.0*
Matches 80; Conservative
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A; Residues: 1-160 < DOW>
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ò 셤 ð 셤 ð 셤 human

Length 158;

Score 157; DB 1; Pred. No. 1.4e-06;

16.6%;

Query Match Best Local Similarity

49 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108

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Nicontains: glicentin-related peptide; glucagon; glucagon-37 (oxyntomodulin); glucagon-1 C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; States Cavia porcellus (guinea pig)
C; States Cavia porcellus (guinea pig)
R; Seino, S.; Welsh, M.; Bell, G.I.; Chan, S.J.; Steiner, D.F.
R; Seino, S.; Welsh, M.; Bell, G.I.; Chan, S.J.; Steiner, D.F.
A; Title: Mutations in the quinea pig preproglucagon gene are restricted to a specific poly. A; Reference number: A24856; MUID:86248118; PMID:3755107
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A,Moeldudes: 53-81 - KHDA.
A,Roedidudes: 53-81 - KHDA.
A,Grossa-references: UNIPARC:UPI00001734FD
R,Conlon, J.M.; Hansen, H.F.; Schwartz, T.W.
R,Conlon, J.M.; Hansen, H.F.; Schwartz, T.W.
A,Fitle: Primary structure of glucagon and a partial sequence of oxyntomodulin (glucagon A,Reference number: A60323; MUID:86017849; PMID:4048553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A/MOJECULE type: protein
A/Residues: 53-81 <CON>
A/Residues: 53-81 <CON
A/Residues: 53-81 <CON
A/Residues: 53-81 <CON
A/Residues: 53-81 <CON
C/SUperfamily: glucagon
C/SUperfamily: glucagon
C/SUperfamily: glucagon
C/Reywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancre
F;1-20/Domain: signal sequence #status predicted <PGC>
F;21-50/Region: glicentin-related peptide #status predicted
F;53-89/Product: glucagon-37 (oxyntomodulin) #status experimental <GCN>
F;53-89/Product: glucagon-1ike peptide | #status predicted <GLI>
F;99-127/Product: glucagon-like peptide | #status predicted <GLI>
F;146-178/Product: glucagon-like peptide 2 #status predicted <GLI>
F;146-178/Product = midated carboxyl end (Arg) (amide in mature form from following gl
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N;Contains: glicentin; glicentin-related polypeptide (GRPP); glucagon; glucagon-like per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ke peptide 1 (tGLP1)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A24377; A44197; A30875; A32614; A01541; S23309
R;White, J.W.; Saunders, G.F.
Nucleic Acids Res. 14, 4719-4730, 1986
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                                                                                                                                  Gaps
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A; Residues: 1-180 <BSI>
A; Cross-references: UNIPROT: PO5110; UNIPARC: UPI000012B82C; DDBJ: D000
R; Huang, C.G.; Bng, J.; Pan, Y.C.E.; Hulmes, J.D.; Yalow, R.S.
Diabetes 35, 508-512, 1986
A; Title: Guinea pig glucagon differs from other mammalian glucagons.
A; Reference number: A23849; MUID: 86165412; PMID: 3956884
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                                    Length 180;
                                    16.6%; Score 157; DB 1;
96.8%; Pred. No. 1.6e-06;
iive 0; Mismatches 1.
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Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                98 HAEGTFTSDVSSYLEGQAAKEFIAWLVKGRG 128
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96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glucagon precursor - guinea pig
N;Alternate names: oxyntomodulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.8
Matches 30; Conservative
                                                                                                                         30; Conservative
                                        Query Match
Best Local Similarity
Matches 30; Conserv
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NiContains: glicentin-related peptide; glucagon; glucagon-like peptide 1; glucagon-like
C; Species: Mesoricctus auratus (golden hamster)
C; Date: 13-Unn-1983 #sequence_revision 13-Unn-1983 #text_change 20-Mar-1998
C; Accession: A01539
R; Bell, G.I.; Santerrer, R.F.; Mullenbach, G.T.
Nature 302, 716-718, 1983
A; Title: Hamster preproglucagon contains the sequence of glucagon and two related peptid
A; Recession: A01539; MUD:83167563; PMID:6835407
A; Accession: A01539
A; Molecule type: mRNA
A; Residues: 1-180 *BEL>
A; Accession: A01539; MUPRC:UPI00001734FE; EMBL:J00059
A; Colomain: Signal sequence #status predicted *SIG>
C; Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancre
F; 1-20/Domain: signal sequence #status predicted *GGN>
F; 21-180/Product: glucagon #status predicted *GGN>
F; 21-180/Product: glucagon-like peptide 1 #status predicted *GLI>
F; 146-180/Product: glucagon-like peptide 2 #status predicted *GLI>
F; 146-180/Product: glucagon-like peptide 2 #status predicted *GLI>
F; 146-180/Product: glucagon-like peptide 2 #status predicted *GLI>
F; 127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                            NyContains: glicentin-related peptide; glucagon; glucagon-like peptide 1; glucagon-like (Species Bos primiganius taurus (cattle)
C; Species Bos primiganius taurus (cattle)
C; Species Bos primiganius taurus (cattle)
C; Species Bos primiganius taurus (cattle)
C; Accession: A3370; A32081; A01538
C; Accession: A3370; A32081; A01538
R; Lopez, L.C.; Frazier, M.L.; Su, C.J.; Kumar, A.; Saunders, G.F.
Proc. Natl. Acad. Sci. U.S.A. 80, 5485-5489; 1983
A; Title: Mammalian pancreatic preproglucagon contains three glucagon-related peptides.
A; Medeuce Lype: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Mesiduce 1.180 c.Lop.
A; Title: Amino acid sequence of bovine glucagon.
A; Reference number: A32081; MUID:71166445; PMID:5102927
A; Title: Amino acid sequence of bovine glucagon.
A; Reference number: A92081; MUID:71166445; PMID:5102927
A; Residuces: 53-81 c.RNO
A; Residuces: 53-81 c.RNO
A; Cross-references: UNPARC:UPI000002C586
C; Superfamily: glucagon
A; Cross-references: UNPARC:UPI000002C586
C; Superfamily: glucagon #status predicted c.PGC>
F; 21-180/Product: proglucagon #status predicted c.PGC>
F; 21-180/Product: glucagon-like peptide: 1 #status experimental c.PGN>
F; 21-180/Product: glucagon-like peptide: 1 #status experimental c.PGN>
F; 88-120, Froduct: glucagon-like peptide: 1 #status experimental c.PGN>
F; 88-120, Froduct: glucagon-like peptide: 1 #status experimental c.PGN>
F; 88-120, Froduct: glucagon-like peptide: 1 #status experimental c.PGN>
F; 88-120, Froduct: glucagon-like peptide: 1 #status experimental c.PGN>
F; 88-120, Froduct: glucagon-like peptide: 1 #status experimental c.PGN>
F; 88-120, Froduct: glucagon-like peptide: 1 #status experimental c.PGN>
F; 88-120, Froduct: glucagon-like peptide: 1 #status experimental c.PGN>
F; 88-120, Froduct: glucagon-like peptide: 1 #status experimental c.PGN>
F; 88-120, Froduct: glucagon-like c.PGN>
F; 8
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C; Superfamily: glucagon
C; Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancre
F;1-20/Domain: aignal sequence #status predicted <816>
F;21-180/Product: proglucagon #status predicted <PGC>
F;21-50/Region: glicantin-related peptide #status predicted
F;3-3-41/Product: glucagon #status experimental <GCI>
F;98-127/Product: glucagon-like peptide 1 #status experimental <GLI>
F;146-178/Product: glucagon-like peptide 2 #status predicted <GLI>
F;146-178/Product: glucagon-like peptide 2 #status predicted corm from following gl
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16.6%; Score 157; DB 1;
Best Local Similarity 96.8%; Pred. No. 1.6e-06;
Matches 30; Conservative 0; Mismatches 1
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                                                                                                                                       2 HGEGTFTSDVSSYLEGOAAKEFIAWLVKGRG 32
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0; Mismatches
30; Conservative
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Nicontains: glicentin-related peptide; glucagon; glucagon-like peptide 1; glucagon-like C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: A2-Sep-1987 #sequence-revision 30-Sep-1987 #text_change 09-Jul-2004
C; Accession: A22655; A25190; A44198
R; Heinrich, G.; Gros, P.; Habener, J.F.
A; Biol. Chem. 259; 14062-14087; 1984
A; Title: Glucagon gene sequence: four of six exons encode separate functional domains on A; Reference number: A22655; MUID:85054833; PMID:6094539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross.tuter. 1-100 cna.
A; Cross.tuter. 2-100 cna.
A; Cross.tuter. 2-100 cna.
A; Cross.tuter. 2-100 cna.
A; Cross.tuter. 2-100 cna.
A; Note: the authors translated the codon TrG for residue 10 as Glu and ACC for residue
B; Mojsov, S.; Heinrich, G.; Wilson, I.B.; Ravazzola, M.; Orci, L.; Habener, J.F.
J. Biol. Chem. 251, 11880-11889, 1986
A; Title: Preproglucagon gene expression in pancreas and intestine diversifies at the leval accession: A25190
A; Reference number: A25190
A; Atatus; not compared with conceptual translation
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C; Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancr-
C; Keywords: amidated carboxyl end; carbohydrate wetabolism; duplication; hormone; pancr-
F; 1-20/Domain: signal sequence #status predicted <PGC>
F; 21-180/Product: proglucagon #status predicted <PGC>
F; 53-81/Product: glucagon #status predicted <PGC>
F; 59-127/Product: glucagon-like peptide | #status predicted <PGL>
F; 146-180/Product: glucagon-like peptide | #status predicted <PGL>
F; 1127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following g
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N;Contains: glicentin-related peptide; glucagon; glucagon-like peptide 1; glucagon-like
N;Contains: glicentin-related peptide; glucagon; glucagon-like peptide 1; glucagon-like
C;Specias: Octodon degus (degu)
C;Specias: 01-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: C36118
R;Nishl, M.; Steiner, D.F.
Mol. Endocrinol. 4, 1192-1198, 1990
A;Title: Cloning of complementary DNAs encoding islet amyloid polypeptide, insulin, and A;Reference number: A36118; MUID:91155952; PMID:2293024
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R;Heinrich, G.; Gros, P.; Lund, P.K.; Bentley, R.C.; Habener, J.F.
Bandocrinology 115, 216-2181, 1984
A;Htle: Pre-proglucagon messenger ribonucleic acid: nucleotide and encoded amino acid A;Reference number: A44198; MUID:85051023; PMID:6548696
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                           glucagon precursor - rat
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A, Molecule type: DNA
A, Residues: 1-180 <HEI>
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A;Molecule type: mRNA
A;Residues: 1-180 <HE2>
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A; Residues: 1-180 <MOJ>
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A;Title: Structure of the human glucagon gene.

A;Reference number: A24377; MUID:86259053; PMID:3725587

A;Rocession: A24377

A;Residues: 1-180

A;Residues: 1-180

A;Cross-references: UNIPROT:P01275; UNIPARC:UPI000012B832; GB:X03991

R;Rell, G.I.; Sanchez-rescador, R.; Laybourn, P.J.; Najarian, R.C.

Nature 304, 368-371, 1983

A;Ritle: Exon duplication and divergence in the human preproglucagon gene.

A;Recence number: A44197; MUID:83271477; PMID:6877358

A;Rocession: A44497

A;Rocession: A44497

A;Rocessidues: 1-179

A;Rocessidues: L-179

A;Rocessidues: L-179

A;Rocessidues: L-179

A;Rocessidues: L-179

A;Rocessidues: L-13475-13478, 1988

A;Title: Glucagon gene expression in vertebrate brain.

A;Reference number: A30875; MUID:88330860; PMID:2901414

A;Rocession: A-106-106

A;Rocession: A-106

A;Rocession: 
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A; Introns: 31/2; 85/2; 131/2; 179/2

C; Superfamily: glucagon

F; 11-20/Domain: signal sequence #status predicted <SIG>
F; 11-20/Product: proglucagon #status experimental <GLN>
F; 11-80/Product: glicentin-related polypeptide #status predicted <GRPP>
F; 11-80/Product: glicentin-related polypeptide #status experimental <GLN>
F; 11-80/Product: glicagon #status experimental <GCN>
F; 11-80/Product: glicagon #status experimental <GLN>
F; 11-80/Product: glicagon #status experimental <GLN>
F; 11-80/Product: glicagon-like peptide 1 #status experimental <GLN>
F; 11-80/Product: glicagon-like peptide 2 #status experimental <GLN>
F; 11-80/Product: glicagon-like peptide 2 #status predicted <GLN>
F; 11-80/Product: glicagon-like &GNN
F; 11-80/Product:
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A; Residues: 1-180 < DRU>
A; Cross-references: UNIDARC: UPIO00012B832; GB:J04040; NID:g183269; PIDN:AAA52567.1; PID:
A; Cross-references: UNIDARC: UPIO00012B832; GB:J04040; NID:g183269; PIDN:AAA52567.1; PID:
J. Biol. Chem. 264, 12826-12829, 1989
A; Fitle: Complete sequences of glucagon-like peptide-1 from human and pig small intestin
A; Reference number: A92732; MUID:89327238; PMID:2753890
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Crosd-references: UNIPARC:UPI000002C586
B;Tsugita, A.; Takamoto, K.; Kamo, M.; Iwadate, H.
R;Tsugita, A.; Takamoto, K.; Kamo, M.; Iwadate, H.
A;Title: C-terminal sequencing of protein. A novel partial acid hydrolysis and analysis
A;Reference number: S23188; MUID:92298996; PMID:1606956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UP100002C586
C;Comment: In pancreatic alpha-cells, proglucagon is processed to glicentin-related poly
stinal L cells, proglucagon is processed to truncated glucagon-like peptide 1, glucagon-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 98-127 <ORS>
A; Cross=references: UNIPARC:UPI0000032E2A
R; Thomsen, J: Ritiansen, K.; Brunfeldt, K.; Sundby,
FBBS Lett. 1, 315-319, 1972
A; Title: The amino acid sequence of human glucagon.
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A,Gene: GDB:GCG
A,Cross-references: GDB:119265; OMIM:138030
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A; Reference number: A91373
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A, Molecule type: protein
A, Residues: 53-81 <TSU>
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Best Local Similarity
Matches 30; Conserv
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A; Molecule type: mRNA A; Residues: 1-180 <NIS> A, Accession: C36118

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Gaps

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1; Indels

16.6%; Score 157; DB 1; 96.8%; Pred. No. 1.6e-06; 0; Mismatches

Conservative

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Search completed: Decemb
Job time: 30.4355 secs
                                           A; Accession: A60836
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Glucagon precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house)
C;Accession: A57294; A4903
R;Rothenberg, M.E.; Eilertson, C.D.; Klein, K.; Zhou, Y.; Lindberg, I.; McDonald, J.K.;
J. Biol. Chem. 270, 10136-10146; 1995
A;Title: Processing of mouse proglucagon by recombinant prohormone convertase 1 and immu A;Reference number: A57294
A;Title: Processing of mouse proglucagon by recombinant prohormone convertase 1 and immu A;Reference number: A57294
A;Status: preliminary
A;Residues: 1-180 cROT-
A;Cessidues: 1-180 cROT-
A;Cross-references: UNIPROT:P55095; UNIPARC:UPI000000192D; EMBL:Z46845; NID:g599880; PIC
C;Superfamily: glucagon
C;Superfamily: quicagon
C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas
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                             C;Superfamily: glucagon
C;Superfamily: glucagon
C;Reywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancre
C;Reywords: amidated carboxyl end; carbohydrate willow
C;Reywords: amidated carboxyl enditted cysto-
F;12-180/Product: proglucagon #status predicted cysto-
F;33-81/Product: glucagon #status predicted cysto-
F;38-12/Product: glucagon-like peptide 1 #status predicted cysto-
F;18/Product: glucagon-like peptide 2 #status predicted cysto-
F;112/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl
Cross-references: UNIPROT: P22890; UNIPARC: UPI000012B839; GB:M57688; NID: 9202467; PIDN:
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N;Contealns: glucagon; glucagon-like peptide 1
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1991 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: 809922; A92189; A60836; A01542
R;Hasesgawa, S.; Terazono, K.; Nata, K.; Takada, T.; Yamamoto, H.; Okamoto, H.
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Best Local Similarity
Matches 30; Conserv
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Matches 30; Conserv
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A;Cross-references: UNIPARC:UPI000012B830
C;Superfamily: glucagon
C;Superfamily: glucagon
C;Superfamily: glucagon
C;Superfamily: glucagon
F;1-22/Domain: signal sequence #status predicted <SIGs
F;23-151/Product: proglucagon #status predicted <PGCs
F;55-83/Product: glucagon #status experimental <GGNs
F;55-83/Product: glucagon #status experimental <GGNs
F;118-147/Product: glucagon-like peptide 1 #status predicted <GLI>F;118-147/Product: glucagon-like peptide 1 #status predicted <GII>F;118-147/Product in mature form from following g]
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R;Irvin, D.M.; Wong, J.
R;Irvin, D.M.; Wong, J.
Rirvin, D.M.; Wong, J.
A;Title: Trout and chicken proglucagon: alternative splicing generates mRNA transcripts
A;Reference number: A55895; MUID:95295739; PMID:7776976
A;Accession: 151301
A;Accession: Island
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPROT: P01277; UNIPARC: UPI000012B82E; GB:S78477; NID:9999386; PIDN
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| Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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A; Reference number: A60836; MUID: 88113418; PMID: 2828209
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Pred. No. 2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 HAEGIYTSDITSYLEGQAAKEFIAWLVNGRG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 HGEGTFTSDVSSYLEGQAAKEFIAWLVKGRG 32
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83.9%;
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Best Local Similarity 83.9
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 83.9
Matches 26; Conservative
                                                             A; Molecule type: protein A; Residues: 55-83 < HUA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: glucagon C; Keywords: duplication
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Sequence 4247, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
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Sequence 4247, Ap
Sequence 18, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, 8 Sequence 16, 8 Sequence 123, Sequence 14, 8 Sequence 147, 8 Sequence 122,
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1 MHGEGTFTSDVSSYLEGQAA......VKCEGISLLAQNTSHHHHH 176
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6_COMB.pep:*
(cgn2_6/ptodata/1/iaa/H_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-09-109-109-16
US-09-209-109-16
US-09-997-792D-16
US-09-997-792D-14
US-09-997-792D-14
US-09-258-750-14
US-09-258-750-15
US-09-258-750-16
US-09-258-750-16
US-09-298-111-16
US-09-398-111-16
US-09-398-111-16
US-09-398-111-16
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US-09-614-847-112
US-09-614-847-113
                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                   572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         OM protein - protein search, using sw model
                                                                                                                                                               Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                         US-10-611-655-10
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Match Length DB
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Perfect score:
                                                                                                                                                    Scoring table:
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                                                                                                                                                                                      Searched:
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Sequence 11168

Sequence 11168

Sequence 11168

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WINDER: 05/241,755

PRIOR REPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSONVTVLRDKLVKCEGISLLAQN 168
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1, Appli
20, Appli
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                          Sequence 3, Ar
Sequence 3, Ar
Sequence 20, Ar
Sequence 21, Ar
Sequence 1, Ar
Sequence 2, Ar
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99.2%; Pred. No. 2.2e-52;
iive 1; Mismatches 0; Indels
US-09-997-792A-13
US-08-095-162-3
US-08-470-220A-3
US-08-967-374-3
US-08-961-405A-1
US-09-258-750-22
US-09-258-750-21
US-09-915-918A-1
US-09-915-918A-1
US-09-915-918A-1
US-09-33-618B-2
US-09-623-618B-2
US-09-33-415-3
US-09-33-415-3
US-09-33-415-3
US-09-33-415-3
US-09-391-3
US-09-391-3
US-09-391-3
US-09-398-111-20
US-09-398-111-20
US-09-398-111-21
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Best Local Similarity 99.2
Matches 121; Conservative
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us-10-611-655-10.rai

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEPSLTRETKKHVLPGTVGVPEHTYRSRTN 79
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR PILING DATE: 1999-02-26
SOFTWARE PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SSG ID NO 4247
LENGTH: 105
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41.0%; Score 387; DB 2; Length 105;
Best Local Similarity 87.1%; Pred. No. 1.8e-29;
Matches 74; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KURIYAMA, Magato
APPLICANT: KURIYAMA, Magato
APPLICANT: KOYAMA, Magato
APPLICANT: KOYAMA, No. 5861284uyuki
APPLICANT: KOYAMA, No. 5861284uyuki
APPLICANT: FUNCUDA, TSUNGHIAKO
TITILE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
TITILE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-PREE
CORRESPONDENCE ADDRESS: 37
CORRESPONDENCE ADDRESS:
STREET: 130 WATER STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                         FEATURE:

NAME/KEY: SIGNAL

COTATION: -19..-1

CTHER INFORMATION: SCOTE 11.7

OTHER INFORMATION: Seq IALLITULQVSRG/QK
US-09-513-999C-4247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 FISKYHMKVLYLSAFTSKDEGTYTC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTENG VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,709
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: 07/838,857
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESULCK S
REGISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-835-231-18; Sequence 18, Application US/08835231 Patent No. 5861284; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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REPERENCY DOCKEY NAMERS: 4114-FWC
TELECOMMUTCATION INFORMATION:
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TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
SEQUENCE CHARACTERISTICS:
MATCHES SECONDAMENT INFORMATION:
MATCHES SECONDAMENT INFORMATION:
APPLICANT: NISTINAMA, MASSON
SECONDAMENT INSINIANA, OSSAN
APPLICANT: NISTINAMA, MASSON
SECONDAMENT INSINIANA, OSSAN
APPLICANT: NISTINAMA, MASSON
SECONDAMENT INSINIANAMA, OSSAN
APPLICANT: NOTHAN, NO. 632 PRODUCTING A SICLOGICCALLY
APPLICANT: NOTHAN, NO. 633 PRODUCTING A SICLOGICCALLY
APPLICANT: NOTHAN, NO. 634 PRODUCTING A SICLOGICCALLY
APPLICANT: NOTHAN, NO. 641
APPLICANT: NOTHAN, NO. 641
APPLICANT: NOTHAN, NO. 641
APPLICANT: NOTHAN, NO. 641
APPLICANTION NUMBER: 07(33,637)
APPLICANT: NOTHAN, NO. 641
APPLICANTION NUMBER: 07(33,637)
APPLICANT
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; OTHER INFORMATION: Description of Artificial Sequence: Gly8-GLP-1(7-37) US-09-614-847-123
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Batent No. 6528486

GENERAL INPORMATION:
APPLICANT: Laren, Bjarne Due
APPLICANT: Mikkelsen, Jens Mollgaard
APPLICANT: Neve, Soren
ITLE OF INVENTION: NOVEL PEPTIDE AGONISTS OF GLP-1 ACTIVITY
FILE REPERRICE: 55511(45487)
CURRENT APPLICATION NUMBER: US/09/614,847

CURRENT FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: US 60/143,591
PRIOR PILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 153

SOFTWARE: Patentin Ver. 2.1

LENGTH: 32
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OTHER INFORMATION: Lys(palmitoyl)
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Gly8-Glp-1(7-36)-Lys37(palmitoyl)(Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 31;
                                                                                 Query Match
17.3%; Score 163; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 31; Conservative 0; Mismatches 0; Indels
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US-09-997-792A-14

Sequence 14, Application US/09997792A

Sequence 14, Application US/09997792A

Sequence 14, Application US/09997792A

GENERAL INFORMATION:

APPLICANT: BLI LILLY and COMPANY

TITLE OF GLUCANTION:

TITLE OF THE REPERENCE: X-10242A

CURRENT APPLICATION NUMBER: US/09/997,792A

CURRENT APPLICATION NUMBER: US 60/069,728

PRIOR APPLICATION NUMBER: US 60/069,728

PRIOR PILING DATE: 1997-12-16

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.1

LENGTH: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Synthetic Construct US-09-997-792A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-614-847-147
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Fatent No. 6528486

GENERAL INFORMATION:
APPLICANT: LARGEMATION:
APPLICANT: Mikkelsen, Jens Mollgaard
APPLICANT: Newe, Soren
TITLE OF INVENTION:
FILE REFERENCE: 55511(45487)
CURRENT APPLICATION NUMBER: US/09/614,847

CURRENT APPLICATION NUMBER: US 60/143,591
FRIOR PILING DATE: 1999-07-13
FRIOR PLING DATE: 1999-07-13
SOFTWARE PATENTIN VET. 2.1
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                            Query Match
18.4%; Score 174; DB 2; Length 176;
Best Local Similarity 76.6%; Pred. No. 6.4e-09;
Matches 36; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MHAEGTFTSDVSSYLEGQAAKEFIAWLVKGRGCPEDGGSGAPPPGHF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 31;
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Patent No. 6380357
GENERAL INFORMATION:
APPLICANT: Hermeling, Ronald
APPLICANT: Hoffmann, James
APPLICANT: Narasimhan, Chakravarthy
TILLS OF INVENTION: GUCAGON-LIKE FEPTIDE-1 CRYSTALS
FILE REFERENCE: X-10242
CURRENT APPLICATION NUMBER: US/09/209,799D
CURRENT APPLICATION NUMBER: US/09/209,799D
NUMBER OF SEG ID NOS: 29
NUMBER OF SEG ID NOS: 29
SOFTWARE: PatentIn version 3.0
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17.3%; Score 163; DB 2; I
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 31; Conservative 0; Mismatches 0;
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             SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                 FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial
                                                                                                                                                                                         ANTI-SENSE: NO
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LENGTH: 31
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Fatent No. 6268343
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HUUSFELDT, PER OLAF
APPLICANT: HUUSFELDT, PER OLAF
APPLICANT: HUUSFELDT, PER PRANKLIN
TITLE OF INVENTION: GLP-1 DERIVATIVES
FILE REFERENCE: 4790.500
CURRENT APPLICATION NUMBER: US/09/258, 750A
CURRENT APPLICATION NUMBER: 08/918, 810
EARLIER APPLICATION NUMBER: 08/918, 810
EARLIER FILING DATE: 1997-08-26
EARLIER FILING DATE: 1997-01-24
EARLIER PILING DATE: 1997-01-24
EARLIER PILING DATE: 1997-01-25
EARLIER PILING DATE: 1997-01-25
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EARLIER FILING DATE: 1997-01-25
EARLIER FILING DATE: 1997-01-24
NUMBER OF SEQ ID NOS: 96
SEQITWARE: FASTESEQ for Windows Version 3.0
SEQ ID NO 15
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Patent No. 6268343
GENERAL INFORMATION:
APPLICANT: RNUDSEN, LISELOTTE BJERRE
APPLICANT: HUUSFELDT, PER OLAF
APPLICANT: HUUSFELDT, PER PRANKLIN
TITLE OF INVENTION: GLP-1 DERIVATIVES
FILE REFERENCE: 4790.500
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 08/918,810
ERALIER FILING DATE: 1997-08-26
EARLIER FILING DATE: 1997-01-24
EARLIER FILING DATE: 1997-01-25
EARLIER FILING DATE: 1997-01-25
EARLIER FILING DATE: 1997-01-25
EARLIER FILING DATE: 1997-01-25
EARLIER FILING DATE: 1997-01-26
EARLIER FILING DATE: 1997-01-26
EARLIER FILING DATE: 1997-01-26
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 31
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ORGANISM: Artificial Sequence
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Best Local Similarity 96.81
Matches 30; Conservative
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Sequence 122, Application US/09614847

Patent No. 6528466

GENERAL INFORMATION:

APPLICANT: Latenen, Blarne Due
APPLICANT: Mikkeleen, Jens Mollgaard
APPLICANT: Neve, Soren

TITLE OF INVENTION: NOVEE PEPTIDE AGONISTS OF GLP-1 ACTIVITY
FILER REFERENCE: 5551, 645487)

CURRENT APPLICATION NUMBER: US/09/614,847

CURRENT PILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/143,591

PRIOR APPLICATION NUMBER: US 60/143,591

PRIOR PILING DATE: 1999-07-13

SOFTWARE: PatentIN Ver. 2.1

LENGTH: 37
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; OTHER INFORMATION: Gly8-GLP-1(7-37)-Lys6
US-09-614-847-122
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Pred. No. 1.6e-08;
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July 10.

US-09-58-750-14

Sequence 14, Application US/09258750A

Patent No. 6268343

GENERAL INFORMATION:
APPLICANT: KNUDSEN, LISELOTTE BJERRE
APPLICANT: HUUSTELDT, PER OLAF

TITLE OF INVENTION: GLP-1 DERIVATIVES
FILE REFRERNCE: 4790-500

CURRENT APPLICATION NUMBER: US/09/258,750A

CURRENT APPLICATION NUMBER: US/09/258,750A

CURRENT APPLICATION NUMBER: 08/918,810

EARLIER PILING DATE: 1997-08-26

EARLIER FILING DATE: 1997-01-24

EARLIER FILING DATE: 1997-01-25

EARLIER FILING DATE: 1997-01-24

EARLIER FILING DATE: 1997-01-24

NUMBER OF SEQ ID NOS: 96

SOFTWARE FILING DATE: 1997-01-24

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 14

LENGTH: 31
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                                                                                     1 HGEGTFTSDVSSYLEGOAAKEFIAWLVKGRG 31
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96.8%;
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ORGANISM: Artificial Sequence
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; OTHER INFORMATION: mutagen
US-09-258-750-14
  31; Conservative
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Best Local Similarity
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  Matches
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RESULT 15
US-09-398-111-15
is Sequence 15. Application US/09398111
Patent No. 6458924
i GENERAL INFORMATION:
APPLICANT: KNUDSELDT, PER OLAF
APPLICANT: HUUSFELDT, PER OLAF
ITILE OF INVENTION: GLP-1 DERIVATIVES
FILE REFERENCE: 4790.500
CURRENT APPLICATION NUMBER: US/09/398,111
CURRENT FILING DATE: 1999-09-16
PRIOR PILING DATE: EARLIER FILING DATE: 1997-04-26
PRIOR PLILING DATE: EARLIER FILING DATE: 1997-01-24
PRIOR PLILING DATE: EARLIER FILING DATE: 1997-01-24
PRIOR PLILING DATE: EARLIER FILING DATE: 1997-01-25
PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-24
NUMBER OF SEQ ID NOS: 96
PROFFMARE: FASISEQ FOR Windows Version 3.0
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16.9%; Score 160; DB 2; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.6e-08;
Matches 30; Conservative 1; Mismatches 0; Indels
16.9%; Score 160; DB 2; Length 31; 96.8%; Pred. No. 1.6e-08; ive 1; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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                                Best Local Similarity 96.8
Matches 30; Conservative
        Query Match
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Patent No. 6438024

GENERAL INFORMATION:

APPLICANT: KNUDSEN, LISELOTTE BJERE

APPLICANT: HUUSFELDT, PER CLAF

APPLICANT: NIELSEN, PER FRANKLIN

TITLE OF INVENTION: GLP-1 DERIVATIVES

FILE REFERENCE: 4790.500

CURRENT APPLICATION NUMBER: US/09/398,111

CURRENT APPLICATION NUMBER: EALLER APPLICATION NUMBER: US/08/918,810A

PRIOR APPLICATION NUMBER: EALLER APPLICATION NUMBER: G0/035,905

PRIOR FILING DATE: EARLER FILING DATE: 1997-01-24

PRIOR FILING DATE: EARLER FILING DATE: 1997-01-24

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: G0/036,226

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: G0/036,226

PRIOR PILING DATE: EARLER FILING DATE: 1997-01-24

PRIOR PILING DATE: EARLER FILING DATE: 1997-01-24

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FASTER FILING DATE: 1997-01-24

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 14

LENGTH: 31

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LENGTH: 31
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16.9%; Score 160; DB 2; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.6e-08;
Matches 30; Conservative 1; Mismatches 0; Indels
                                                                                    Length 31;
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Patent No. 6380357
GENERAL INFORMATION:
APPLICANT: Hermaling, Ronald
APPLICANT: Hermaling, Ronald
APPLICANT: Hermaling, Chakravarthy
TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS
FILE REFERENCE: X-10242
CURRENT APPLICATION WUMBER: US/09/209,799D
CURRENT FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
SEQ ID NO 28
LENGTH: 31
                                                                                    Query Match 16.9%; Score 160; DB 2; Best Local Similarity 96.8%; Pred. No. 1.6e-08; Matches 30; Conservative 1; Mismatches 0
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ORGANISM: Artificial Sequence
     ; OTHER INFORMATION: mutagen US-09-258-750-16
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) OTHER INFORMATION:
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Sequence 6, Appli
Sequence 220, Appl
Sequence 220, App
Sequence 220, App
Sequence 220, App
Sequence 66, Appl
Sequence 66, Appl
Sequence 1149, App
Sequence 1184, App
Sequence 1384, App
Sequence 1624, App
Sequence 20, Appli
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532.965 Million cell updates/sec
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                                                                                                                                                                                                            6, 2005, 10:32:17 ; Search time 137.979 Seconds
                                                                                                                                                                                                                                                                                                                                 US-10-611-655-10
944
I MHGEGTFTSDVSSYLEGQAA.....VKCEGISLLAQNTSHHHHHH 176
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

1: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

1: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 QSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSKTNFTSKYHMKVLYL 120
                                                           49895, A
84, Appl
13, Appl
2, Appli
2, Appli
4, Appl
131, App
417, App
613, Ap
600, Ap
600, Ap
1600, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQNTSHHHHHH 176
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GENERAL INFORMATION:
FILE REPERROR: 6663-026; CURRENT FAPLICATION NUMBER: US/10/611,655; CURRENT FILING DATE: 2003-06-30; NUMBER OF SEQ ID NOS: 13; SOFTWARE: PastSEQ for Windows Version 4.0; SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 944; DB 5; Length 176;
Best Local Similarity 100.0%; Pred. No. 7.2e-70;
Matches 176; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/10611655
; Publication No. US20040266993A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
; FILE REFERENCE: 66663-026
; CURRENT APPLICATION NUMBER: US/10/611,655
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASELSEQ for Windows Version 4.0
US-10-433-108-23
US-10-433-108-25
US-10-433-108-28
US-10-950-763-49895
US-10-97-700-84
US-10-931-108-22
US-10-433-108-22
US-09-969-748C-2
US-10-775-180-131
US-10-775-180-611
US-10-775-204-1623
US-10-775-204-1623
US-10-775-204-1609
US-10-775-204-1609
US-10-775-180-600
US-10-775-180-600
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US-10-775-180-600
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 VLFGTVGVPEHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 VLFGTVGVPEHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVT 308
                                                                                                                                                                                                                                                     249 VLFGTVGVPEHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVT 308
                                                                                                                                                                                                                                                                                                             91 VLPGTVGVPEHTYRSRTNPTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVT 150
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                                                                                                                                                                                    Gaps
                                  ; OTHER INFORMATION: chimeric ThyOx carrier polypeptide containing ; OTHER INFORMATION: erythropoietin US-10-611-655-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 334;
                                                                                                                                            Length 334;
                                                                                                                                                                                  Indels
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Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 146; Conservative 0; Mismatches 0;
                                                                                                                                       Query Match
83.4%; Score 787; DB 5; L
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 146; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                             151 VLRDKLVKCEGISLLAQNTSHHHHHH 176
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Publication No. US20030017157A1
GENERAL INFORMATION:
TYPE: PRT ORGANISM: Artificial Sequence
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US-10-611-655-8
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US-10-611-655-8
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APPLICANT: Berd St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kennech Kinzler
IIIE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134

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109 FISKYHMKVLYLSAFISKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSONVTVLRDKLVKCEGISLLAQN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 OKVTSLTACLVDOSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 161;
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publication No. US20040213793A1

GENERAL INPORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: Carson-Walter, Eleanor
APPLICANT: Kincler, Brad
APPLICANT: Kincler, Kenneth
ITILE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179

CURRENT APPLICATION NUMBER: US/10/474,794

CURRENT APPLICATION NUMBER: 60/282,850
PRIOR PILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
PRIOR PLING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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100.0%; Pred. No. 1.2e-44;
ative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/224,599
FRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: PASESEQ for Windows Version 3.0
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.5
Best Local Similarity 100.
Matches 122; Conservative
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US-09-918-715-220
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49 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
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                                                                                                                                      109 FISKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSONVTVLRDKLVKCEGISLLAQN 168
                                                                                         20 OKVTSLTACLVDOSLRLDCRHENTSSSPIQYBFSLTRETKKHVLFGTVGVPEHTYRSRTN 79
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Publication No. US20040146516A1
GENERAL INFORMATION:
APPLICANT: Utah Ventures
TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
FILE REFERENCE: 27110-715
CURRENT APPLICATION NUMBER: US/10/794,899
CURRENT PILING DATE: 2004-03-05
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
                                             49 OKVTSLIACLVDQSLRLDCRHENTSSPIQYEFSLIRETKKHVLFGTVGVPEHTYRSRIN
Gaps
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Sequence 449, Application US/10287436A

Publication No. US20050202421A1

GENERAL INFORMATION:
TITLE OF INVENTION: METHOD FOR DIGGNOSIS AND TREATMENT OF TITLE OF INVENTION: RHEUMATOD ARTHRITIS

FILE REFERENCE: 10872.514696

CURRENT APPLICATION NUMBER: US 60/336,220

PRIOR APPLICATION NUMBER: US 60/336,220

PRIOR PLILING DATE: 2001-10-31

NUMBER OF SEQ ID NOS: 14466

SOFTWARE: FREUENCE OF Windows Version 4.0

SEQ ID NO 449
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Pred. No. 4.5e-44;
1; Mismatches 0; Indels
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Pred. No. 4.5e-44;
0; Indels
1; Mismatches
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    Matches 121; Conservative
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Best Local Similarity
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Best Local Similarity
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LENGTH: 161
TYPE: PRT
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Publication No. US20030021792A1

GENERAL INFORMATION:
APPLICANT: Stevens, Paul W.
TITLE OF INVENTION: TISSUE-SPECIFIC ENDOTHELIAL MEMBRANE
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEINS
TITLE REPERENCE: TPTECH.001A
CURRENT APPLICATION NUMBER: US/10/165,603
CURRENT PILING DATE: 2002-06-07
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 161
                                                                                                                                                                        APPLICANT: BEAG SEC. LOLLA.
APPLICANT: BEAT VOGELSTEIN
APPLICANT: Remeth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILER REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
FRIOR APPLICATION NUMBER: US/09/918,715
PRIOR PLLING DATE: 2000-08-02
PRIOR PLLING DATE: 2000-08-02
PRIOR PLLING DATE: 2000-08-02
PRIOR PLLING DATE: 2000-08-11
PRIOR PLLING DATE: 2000-08-11
PRIOR PLLING DATE: 2000-08-11
PRIOR PLLING DATE: 2000-08-11
PRIOR PLLING DATE: 3000-08-11
PRIOR PLLING DATE: 3000-04-11
SPRIOR PLLING DATE: 3000-04-11
SPRIOR PLLING DATE: 3000-04-11
SPRIOR PLLING DATE: 3580
SOFTWARE: PASTSEQ for Windows Version 3.0
                                                                                           Sequence 220, Application US/10979159
Publication No. US20050142138A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
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US-10-979-159-220
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Best Local Similarity
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Sequence 1, Application US/10611655
Publication No. US20040266993A1
GENERAL INFORMATION:
GENERAL INFORMATION:
1 TITLE OF INVENTION:
1 TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
1 TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
1 TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
2 TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
3 TITLE OF INVENTION: 103-104
3 TITLE OF INVEN
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Best Local Similarity 99.2%;
Matches 121; Conservative
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CORGANISM: Homo sapiens
US-10-106-698-4624
                                                                                             Local Similarity
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   US-09-925-301-1384
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US-10-611-655-1
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                                                               49 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
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Patent No. US20020052308A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: BCT/US00/05882

PRIOR PILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12
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Publication No. US20050202121A1
GENERAL INPORMATION:
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: METHOD APPLICATION NUMBER: US/10/287,436A;
CURRENT FILING DATE: 2002-10-31
PRIOR PAPLICATION NUMBER: US 60/336,220
PRIOR PAPLICATION NUMBER: 2001-10-31
NUMBER OF SEQ ID NOS: 1446
SOFTWARE: PREAESEQ for Windows Version 4.0
SEQ ID NO 1149
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0; Indels
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Pred. No. 4.5e-44;
1; Mismatches 0
1; Mismatches
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Best Local Similarity 99.2%;
Matches 121; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1384
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
Matches 121; Conservative
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ORGANISM: Homo sapiens
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US-09-925-301-1384
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Publication No. US20030109690A1

Sequence 4624, Application US/10106698

Publication No. US20030109690A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polymucleotides and Polypeptide

FILE REFERENCE: PA005P1

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR FILING DATE: 1999-09-29

PRIOR PILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-11-03

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: Patentin Ver. 3.0
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66.7%; Score 630; DB 3; Length 165; 99.2%; Pred. No. 4.6e-44; ive 1; Mismatches 0; Indels
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Pred. No. 4.6e-44;
1; Mismatches 0; Indels
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                                                                                                                                                                                  49 OKVISLIACLVDOSLRLDCRHENISSSPIQYEFSLIREIKKHVLFGTVGVPEHTYRSRIN 108
                                                                                                                                                                                                                                                                     FISKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPI-SSQNVTVLRDKLVKCEGISLLAQ 167
                                                                                                                                                                                                                                                                                             FISKYHMKVLYLSAFISKDEGIYTCALHHSCHSPPILSSONVTVLRDKLVKCEGISLLAQ 139
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                                                                                                                                                                                                          QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEESLTRETKKHVLPGTVGVPEHTYRSRTN 79
                                                                                                                                             Gaps
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                                                                                               Query Match 65.4%; Score 617.5; DB 5; Length 162; Best Local Similarity 98.4%; Pred. No. 4.8e-43; Matches 121; Conservative 0; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.6%; Score 600; DB 4; Length 159; 96.7%; Pred. No. 1.3e-41; Live 1; Mismatches 1; Indel8
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Fublication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 49897, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyeeq. Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2003-06-11
; PRIOR PLICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: 905/40,217
; PRIOR PLILNG DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
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Best Local Similarity 96.74
Matches 118; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
                 TYPE: PRT
ORGANISM: Homo sapiens
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US-10-450-763-49897
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US-10-322-281-20
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LENGTH: 162
                                                  US-10-611-655-1
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49 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
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Pred. No. 4.2e-27;
9; Mismatches 21; Indels
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OTHER INFORMATION: Xaa = X or * as defined in Table 2
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Job time : 138.979 secs
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Best Local Similarity 71.9%;
Matches 92; Conservative
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUBtom
SEQ ID NO 49897
LENGTH: 171
                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                           NAME/KEY: misc_feature
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Sequence 31, Appli
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Sequence 1, Appli
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Sequence 8, Appli
Sequence 12, Appli
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Sequence 1230, Ap
Sequence 1230, Ap
Sequence 1230, Ap
Sequence 1520, Ap
Sequence 1520, Ap
Sequence 1530, Ap
                                                                                                               6, 2005, 10:37:02; Search time 7.35888 Seconds (without alignments) 114.521 Million cell updates/sec
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Sequence 11, P
Sequence 9, Ag
Sequence 31, P
Sequence 7, Ag
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944
1 MHGEGTFTSDVSSYLEGQAA......VKCEGISLLAQNTSHHHHHH 176
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1: /cgn2_6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/PUSI_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*

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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-997-061-3
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US-10-997-061-31
US-10-997-061-31
US-10-997-061-13
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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APPLICANT: Luan, Peng
APPLICANT: Xia, Yuannan
APPLICANT: Sobsard, Mary
APPLICANT: Bossard, Mary
APPLICANT: Bossard, Mary
APPLICANT: Holmquist, Barton
APPLICANT: Bossard, Mary
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
FILE REPERENCE: 1627.03191
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, 100-11-24
CURRENT APPLICATION NUMBER: US/10/997,061
CURRENT APPLICATION NUMBER: US 60/383,214
FRIOR FILING DATE: 2002-05-23
FRIOR APPLICATION NUMBER: US 60/383,214
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LEGGITH: 70
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   11150, Ap
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Pred. No. 1.3e-08;
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US-11-054-515-1150

US-11-054-515-1038

US-11-054-515-1030

US-11-054-515-1037

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US-11-054-515-1046

US-11-054-515-1037

US-11-054-515-1037

US-11-054-515-1031

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US-11-054-515-1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/10997061; Publication No. US20050260701A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.9%;
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ORGANISM: Artificial Sequence
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Matches 32; Conservative
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       JS-10-997-061-28
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Sequence 3, Application US/10997061; Publication No. US20050260701A1; GENERAL INFORMATION:

US-10-997-061-3

APPLICANT: Wagner, Fred W. APPLICANT: Luan, Peng APPLICANT: Xia, Yuannan

48, App

Sequence Sequence Sequence

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APPLICANT: Als, Yuannan
APPLICANT: Bossard, Mary
APPLICANT: Holmquist, Barton
APPLICANT: Holmquist, Barton
APPLICANT: Holmquist, Barton
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
FILE REFERENCE: 1627.003101.
TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
FILE OF INVENTION: WORDER: US/10/997,061
CURRENT PELLING DATE: 2004-11-24
PRIOR FILING DATE: 2003-05-24
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 31
SOFIL ON SEQ ID NOS: 31
SEQ ID NO 9
SEQ ID NO 9
LENGTH: 117
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APPLICANT: Hologuist, Barton
APPLICANT: Merrifield, Edwin H.
APPLICANT: Merrifield, Edwin H.
APPLICANT: Strydom, Daniel
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
FILE REPERENCE: 1627.003101.
CURRENT APPLICATION NUMBER: US/10/997,061
PRIOR APPLICATION NUMBER: US 60/383,14
PRIOR APPLICATION NUMBER: US 60/383,214
PRIOR PILING DATE: 2002-05-23
RIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PRACES OF Windows Version 4.0
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        2 MHAEGTFTSDVSSYLEGQAAKEFIAWLVKGR 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: A synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31, Application US/10997061 Publication No. US20050260701A1 GENERAL INFORMATION:
                                                                                                                                                 Sequence 9, Application US/10997061 Publication No. US20050260701A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1
OTHER INFORMATION: Xaa = T7-tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 75.0 Matches 33; Conservative
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                                                                                                                                                                                                                                    APPLICANT: Wagner, Fred W. APPLICANT: Luan, Peng
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US-10-997-061-31
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APPLICANT: Bossard, Mary
APPLICANT: Holmquist, Barton
APPLICANT: Holmquist, Barton
APPLICANT: Holmquist, Barton
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
ITIER APPLICANT: Restoragen Inc.
ITIER OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
FILE REFERENCE: 1627.0031031
CURRENT APPLICATION NUMBER: US/10/997,061
CURRENT APPLICATION NUMBER: US/10/33/16469
PRIOR FILING DATE: 2004-11-24
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2003-05-24
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PastsEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 31
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APPLICANT: Bossard, Mary
APPLICANT: Bossard, Mary
APPLICANT: Holmquist, Barton
APPLICANT: Holmquist, Barton
APPLICANT: Strydon, Daniel
APPLICANT: Strydon, Daniel
APPLICANT: Strydon, Daniel
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Method for Bnzymatic Production of GLP-1(7-36) Amide Peptides
TITLE TEREBERRE: 1527.031531
CURRENT APPLICATION NUMBER: 105/10/997,061
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16.5%; Score 156; DB 6; Length 277;
Best Local Similarity 96.8%; Pred. No. 1.3e-07;
Matches 30; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.6%; Score 157; DB 6; Length 31; Best Local Similarity 96.8%; Pred. No. 1e-08; Matches 30; Conservative 0; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: PCT/US03/16469

PRIOR FILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: US 60/383,214

PRIOR PILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGIH: 277
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; OTHER INFORMATION: A synthetic peptide US-10-997-061-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: A synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/10997061
Publication No. US20050260701A1
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US-10-997-061-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Magner, Fred W.
APPLICANT: Luan, Peng
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APPLICANT: Bossard, Mary
APPLICANT: Holmquist, Barton
APPLICANT: Holmquist, Barton
APPLICANT: Holmquist, Barton
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
APPLICANT: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
TITIE REPERENCE: 1627.003URS: US/10/997,061
CURRENT APPLICATION NUMBER: US/10/997,061
CURRENT FILING DATE: 2004-01-24
PRIOR PTLING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,214
PRIOR PTLING DATE: 2002-05-24
NUMBER: OF SEQ ID NOS: 31
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                          16.1%; Score 152; DB 6; Length 119; 72.7%; Pred. No. 1.2e-07; rive 1; Mismatches 9; Indel8
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                  CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16469
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,214
PRIOR PILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 119
CURRENT APPLICATION NUMBER: US/10/997,061
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OTHER INFORMATION: A synthetic peptide
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                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 1
; OTHER INFORMATION: Xaa = T7-tag
US-10-997-061-13
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Best Local Similarity 72.74
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Xia, Yuannan
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APPLICANT: Lian, Peng
APPLICANT: Lian, Peng
APPLICANT: Ala, Yuannan
APPLICANT: Bossard, Mary
APPLICANT: Bossard, Mary
APPLICANT: Holmquist, Barton
APPLICANT: Merrifield, Edwin H.
APPLICANT: Merrifield, Edwin H.
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
FILE REFERENCE: 1627.003US1
CURRENT APPLICATION NUMBER: US/10/997,061
CURRENT APPLICATION NUMBER: US/10/803/16469
PRIOR PILING DATE: 2003-05-23
PRIOR PILING DATE: 2003-05-24
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PastSEQ for Windows Version 4.0
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16.4%; Score 155; DB 6; Length 122;
Best Local Similarity 75.0%; Pred. No. 6.7e-08;
Matches 33; Conservative 0; Mismatches 9; Indels
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Pred. No. 1.9e-08;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: A synthetic peptide US-10-997-061-7
                           FEATURE:
OTHER INFORMATION: A synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/10997061
Publication No. US20050260701A1
GENERAL INFORMATION:
                                                                   FRATURE:

NAMB/KSY: SITE
LOCATION: 14

COTHER INFORMATION: Xaa = Peptide 5
US-10-997-061-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/10997061
Publication No. US20050260701A1
GENERAL INFORMATION:
APPLICANT: Wagner, Fred W.
APPLICANT: Ludan, Peng
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Best Local Similarity 93.5%;
Matches 29; Conservative
      ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wagner, Pred W. APPLICANT: Luan, Peng APPLICANT: Xia, Yuannan APPLICANT: Bossard, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Restoragen Inc
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APPLICANT:
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US-10-997-061-7
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Sequence 12, Application US/10997061

Sequence 12, Application US/10997061

Publication No. US20050260701A1

GENERAL INFORMATION:

APPLICANT: Wagner, Fred W.

APPLICANT: Luan, Peng
APPLICANT: Holmquist, Barton

APPLICANT: Holmquist, Edwin H.

APPLICANT: Merrifield, Edwin H.

APPLICANT: Restoragen Inc.

APPLICANT: Restoragen Inc.

TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides

FILE REFERENCE: 1627.003US1

CURRENT APPLICATION NUMBER: PCT/US03/16469

PRIOR APPLICATION NUMBER: PCT/US03/16469

PRIOR APPLICATION NUMBER: PCT/US03/16469

PRIOR PILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 31

SOFTMARE: PRESENCE FOR Windows Version 4.0

SRO ID NO.: SRO ID NOS: 2003-05-24
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TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
FILE REPERENCE: 1627.003US1
FURRENT APPLICATION NUMBER: US/10/997,061
CURRENT FILING DATE: 2004-11-24
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                                                                                                           Gaps
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                                                   16.0%; Score 151; DB 6; Length 34; 96.7%; Pred. No. 3.8e-08; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                            1 HAEGTFTSDVSSYLEGQAAKEFIAMLVKGR 30
                                                                                                                                                         2 HGEGTFTSDVSSYLEGOAAKEFIAWLVKGR 31
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PRIOR APPLICATION NUMBER: PCT/US03/16469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: A synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           j OTHER INFORMATION: Xaa = Hse-lactone
US-10-997-061-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10997061 Publication No. US20050260701A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmquist, Barton
Merrifield, Edwin H.
Strydom, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                        Query Match
Best Local Similarity 96,,,
Best Local 29, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.7
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Luan, Peng
Xia, Yuannan
Bossard, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
US-10-997-061-10
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US-10-997-061-5
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APPLICANT:
APPLICANT:
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LENGTH: 34
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             APPLICANT: Wagner, Fred W.
APPLICANT: Wagner, Fred W.
APPLICANT: Luan, Peng
APPLICANT: Luan, Peng
APPLICANT: Luan, Peng
APPLICANT: Bossard, Mary
APPLICANT: Holmquist, Barton
APPLICANT: Holmquist, Barton
APPLICANT: Strydom, Daniel
TITLE REFERENCE: 1627.0031031
CURRENT APPLICATION NUMBER: US/10/997,061
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,214
PRIOR FILING DATE: 2005-23
PRIOR PRILICATION NUMBER: US 60/383,214
PRIOR FILING DATE: 2005-05-24
NUMBER OF SEQ ID NOS: 31
SOFTWARER: FRAEEC for Windows Version 4.0
SEQ ID NO 4
LENGTH: 31
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APPLICANT: Wagner, Fred W.
APPLICANT: Wagner, Fred W.
APPLICANT: Luan, Peng
APPLICANT: Xia, Yuannan
APPLICANT: Waster, Mary
APPLICANT: Holmquist, Barton
APPLICANT: Berardid, Edwin H.
APPLICANT: Berriffield, Edwin H.
APPLICANT: Strydom, Daniel
APPLICANT: Restoragen Inc.
APPLICANT: Restoragen Inc.
APPLICANT: Restoragen Inc.
APPLICANT: Restoragen Inc.
APPLICANT: Berriffield, Edwin H.
APPLICANT: Berriffield, Edwin H.
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
CURRENT APPLICATION NUMBER: US/10/997,061
CURRENT APPLICATION NUMBER: US/01/93/16469
FRIOR APPLICATION NUMBER: US 60/383,214
FRIOR FILING DATE: 2002-05-23
FRIOR APPLICATION NUMBER: US 60/383,214
FRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 34
TYPE: PRT
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OTHER INFORMATION: A synthetic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 31
; OTHER INFORMATION: Xaa = Gly- NH2
US-10-997-061-4
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APPLICANT: Holmquist, Barton
APPLICANT: Holmquist, Barton
APPLICANT: Merifield, Edwin H.
APPLICANT: Merifield, Edwin H.
APPLICANT: Merifield, Edwin H.
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
FILE REFERENCE: 1677.003US1
CURRENT PAPLICATION NUMBER: US/10/997,061
CURRENT PAPLICATION NUMBER: DCT/US03/16469
PRIOR PHILNG DATE: 2003-05-24
PRIOR FILING DATE: 2003-05-24
PRIOR FILING DATE: 2002-05-24
NUMBER: OF SEQ ID NOS: 31
SOUTHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 30
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US-11-054-515-1480

Sequence 1465, Application US/11054515

Publication No. US2005025532A1

GENERAL INFORMATION:
APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF52.395

PRIOR PERFERENCE: 2005-02-10

PRIOR PELICATION NUMBER: 60/543,296

PRIOR PELICATION NUMBER: 60/580,347

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR PILING DATE: 2001-11-14

PRIOR PILING DATE: 2001-12-19

PRIOR PELICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR PELING DATE: 2001-65-25

PRIOR PELING DATE: 2001-05-25

PRIOR PELING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-03-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 30
OTHER INFORMATION: Xaa = Arg-NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 28; Conserv
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APPLICANT: Wagner, Fred W.
APPLICANT: Luan, Peng
APPLICANT: Luan, Peng
APPLICANT: Luan, Peng
APPLICANT: Stard, Mary
APPLICANT: Boseard, Mary
APPLICANT: Boseard, Mary
APPLICANT: Beserving Barton
APPLICANT: Marrifield, Edwin H.
APPLICANT: Restoragen Inc.
APPLICANT: Strydom, Daniel
APPLICANT: Print Daniel
APPLICANT: Restoragen Inc.
FILER REFERENCE: 167.003U31
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/U803/16469
PRIOR PILING DATE: 2002-05-24
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SSEQ ID NO 8
SSEQ ID NO 8
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15.7%; Score 148; DB 6; Length 31;
Best Local Similarity 93.3%; Pred. No. 6.3e-08;
Matches 28; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Score 148; DB 6; Length 30;
Pred. No. 6.1e-08;
1; Mismatches 1; Indels
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PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,214
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PASICED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: A synthetic peptide US-10-997-061-5
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LOCATION: 31
COTHER INFORMATION: Xaa = Gly-NH2
US-10-997-061-8
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.3%;
Matches 28; Conservative 1
                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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LENGTH: 30
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Search completed: December 6, 2005, 10:48:05 Job time: 7.35888 secs

OM protein - protein search, using sw model

6, 2005, 10:32:12; Search time 164.348 Seconds (without alignments) 470.529 Million cell updates/sec December Run on:

US-10-611-655-10 Perfect score:

944 1 MHGEGTFTSDVSSYLEGQAA.....VKCEGISLLAQNTSHHHHHH 176 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2443163 seqs, 439378781 residues Searched:

Total number of hits satisfying chosen parameters:

2443163

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Geneseq 21:* Database

geneseqp1990s:* geneseqp2000s:* geneseqp1980s:*

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2001s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	101141111111111111111111111111111111111	Adw10192 Chimeric	Adw10190 Erythropo	Adw10188 Chimeric	Abb90744 Human Tum	Abu54451 Human tum	Adp65208 Human Thy	Abo84755 Human can	Adz13572 Human can	Adz13574 Human can	Adz13570 Human can	Aab43939 Human can	Aag73850 Human col	Human	Human	Aay31787 Human Thy		Abg19538 Novel hum	Aaw53480 Rat THY-1	Abb90786 Mouse Tun	Abu54493 Mouse tum	Abo84754 Murine ca	Adz13567 Murine ca	Adw10186 Thy-1 bas	1-114T Ted 001151108
SUMMARIES	91		ADW10192	ADW10190	ADW10188	ABB90744	ABU54451	ADP65208	AB084755	ADZ13572	ADZ13574	ADZ13570	AAB43939	AAG73850	ADW10183	AAY31789	AAY31787	ADK98542	ABG19538	AAW53480	ABB90786	ABU54493	AB084754	ADZ13567	ADW10186	AAY31788
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	Query Match	יומרכוו	100.0	83.4	83.4	67.5	67.5	66.7	66.7	66.7	66.7	66.7	66.7	66.7	65.4	64.0	63.6	57.8	44.9	44.6	43.1	43.1	43.1	43.1	42.2	41.2
	Score	0 100 1	944	787	787	637	637	630	630	630	630	630	630	630	617.5	604	9	546	424	421	406.5	406.5	406.5	406.5	398	389
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Huma		Adf12417 Mouse Thy	Adg39435 Mouse Thy	Aae30917 Val8-GLP-	Adw44109 Glucagon-	Aae30929 Gly8-Glu2	Aae30918 Gly8-Glu2	Aae30927 Gly8-Glu2	Aae30926 Gly8-Glu2		Aae30931 Gly8-Glu2	Abg19536 Novel hum		Aae30925 Gly8-Glu2	Aae30916 Val8-GLP-	Adw45209 K. lactis				Adw45219 K. lactis
AAG00166	AAY31786	ADF12417	ADG39435	AAE30917	ADW44109	AAE30929	AAE30918	AAE30927	AAE30926	AAE30928	AAE30931	ABG19536	ADJ65908	AAE30925	AAE30916	ADW45209	ABP55318	ADL99518	AAE29202	ADW45219
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105	119	114	114	631	71	294	640	284	287	302	287	51	98	272	616	649	290	290	291	646
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41	40	39	39	24	23	23	23	22	22	22	21	21	13	18	18	17	17	17	17	17
387	385	370.5	370.5	233.5	224.5	224.5	220	214	211.5	210.5	206.5	203	182	177	173	168	167	167	167	166.5
25	56	27	28	5	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

ADW10192 standard; protein; 176 AA. RESULT 1 ADW10192

ADW10192; 

(first entry) 24-MAR-2005 Chimeric ThyOx carrier containing glucagon-like peptide 1.

non-immunoglobulin binding polypeptide; selective binding; ThyOx; glucagon-like peptide 1; GLP-1.

Chimeric.

Synthetic.

US2004266993-A1.

30-DEC-2004.

30-JUN-2003; 2003US-00611655.

30-JUN-2003; 2003US-00611655.

(EVAN/) EVANS G A.

Evans GA;

WPI; 2005-047648/05. N-PSDB; ADW10191 New chimeric non-immunoglobulin binding polypeptide comprises immunoglobulin-like domain containing scaffold and exhibits selective binding activity, for producing non-immunoglobulin binding polypeptides with selective binding activity.

Disclosure; SEQ ID NO 10; 45pp; English.

The invention relates to a novel chimeric non-immunoglobulin binding polypeptide. The polypeptide comprises an immunoglobulin-like domain containing scaffold with two or more solvent exposed loops containing different complementarity-determining region (CDR) from a parent antibody inserted into each of the loops and exhibiting selective binding activity toward a ligand bound by the parent antibody. The invention further comprises a chimeric Thyox binding polypeptide, comprising one or more altered immunoglobulin-like domain loop regions of a Thyox family polypeptide or at least one immunoglobulin-like domain containing

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Matches
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        binding polypeptide exhibiting selective binding activity toward a non-Thyox ligand; and a nucleic acid encoding the non-immunoglobulin or Thyox binding polypeptide above. The chimeric non-immunoglobulin binding polypeptide is useful for producing non-immunoglobulin binding polypeptides having selective binding activity toward a predetermined molecule. This sequence represents a chimeric Thyox carrier containing glucagon-like peptide 1 of the invention.
                                                                                                                                                                                                                             QSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTNFTSKYHMKVLYL 120
                                                                                                                                                                                                                                         The invention relates to a novel chimeric non-immunoglobulin binding belypeptide. The polypeptide comprises an immunoglobulin-like domain containing scaffold with two or more solvent exposed loops containing a different complementarity-determining region (CDR) from a parent antibody inserted into each of the loops and exhibiting selective binding activity toward a ligand bound by the parent antibody. The invention further comprises: a chimeric Thyox binding polypeptide, comprising one or more
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                                                                                                                                                                                            1 MHGEGTFTSDVSSYLEGQAAKEFIAWLVKGRGGGGGGGGGGGGGGGGGGGGGCGCTACLVD
                                                                                                                                                                                                                                                                                        SAFTSKDEGTYTCALAHSGHSPPISSQNVTVLRDKLVKCEGISLLAQNTSHHHHHH 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-immunoglobulin binding polypeptide; selective binding; ThyOx;
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                                                                                                                                 Length 176;
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scaffold derived from a ThyOx family polypeptide,
                                                                                                                               100.0%; Score 944; DB 9;
100.0%; Pred. No. 9.6e-85;
                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               Erythropoietin protein, named SuperEpo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, SEQ ID NO 8; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                         ADW10190 standard; protein; 334 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with selective binding
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N-PSDB; ADW10189.
                                                                                                                                           Local Similarity
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                                                                                                        Sequence 176 AA;
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                                                                                                                                                    Matches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                             61
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                                                                                                                               Query Match
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altered immunoglobulin-like domain loop regions of a ThyOx family polypeptide or at least one immunoglobulin-like domain containing scaffold derived from a ThyOx family polypeptide, and a heterologous binding polypeptide exhibiting selective binding activity toward a non ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or Thoinding polypeptide above. The chimeric non-immunoglobulin binding polypeptides having selective binding activity toward a propeptide having selective binding activity toward a predetermined molecule. This sequence represents an erythropoietin protein, named SuperEpo, of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 RGGGGGGGGGGGGGGGGGGGKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLFGTVGVPEHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 VLFGTVGVPEHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSONVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.4%; Score 787; DB 9;
100.0%; Pred. No. 6.5e-69;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLRDKLVKCEGISLLAQNTSHHHHH 176
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hes 146; Conservative
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N-PSDB; ADW10187.
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 334 AA;
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Carson-Walter E, St Croix B,
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                                                                                                                                                                       Sequence 161 AA;
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toward a ligand bound by the parent antibody. The invention further comprises: a chimeric Thyox binding polypeptide, comprising one or more attered immunoglobulin-like domain loop regions of a Thyox family polypeptide or at least one immunoglobulin-like domain containing scaffold derived from a Thyox family polypeptide, and a heterologous binding polypeptide exhibiting selective binding activity toward a non-Thyox ligand; and a nucleic acid encoding the non-immunoglobulin or Thyox binding polypeptide above. The chimeric non-immunoglobulin binding polypeptide having selective binding activity toward a predetermined molecule. This sequence represents a chimeric Thyox carrier containing erythropoietin of the invention.
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                                                                                                                                                                                                                                                            189 RGGGGGGGGGGGGGGGGGGVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKH
                                                                                                                                                                                                                                                                                      VLFGTVGVPEHTYRSRTNFTSKYHMKVLYLSAPTSKDEGTYTCALHHSGHSPPISSQNVT
                                                                                                                                                                                                                                                                                                           249 VLFGTVGVPEHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVT
                                                                                                                                                                                                                                     RGGGGGGGGGGGGGGGGGGKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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                                                                                                                                                                                      Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Tumour Endothelial Marker polypeptide SEQ ID NO 220.
                                                                                                                                                                                                            Indels
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100.0%; Pred. No. 6.5e-69;
ive 0; Mismatches 0;
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11-APR-2001; 2001US-0282850P.
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                                                                                                                                                                                   Query Match 83.4
Best Local Similarity 100.
Matches 146; Conservative
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                                                                                                                                                              Sequence 334 AA
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90749, ABB90749, ABB90749, ABB90749, ABB90749, ABB90769 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antianglogenic activity. They are useful for inhibiting tumour growth, neoanglogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL92042-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92041 and pan-endothelial markers (FEM) ABL92042-ABL92074; and pan-endothelial markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 OKVISLIACLVDQSLRLDCRHENTSSPIQYEFSLIRETKKHVLFGTVGVPEHTYRSRIN
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Tumour endothelial marker; normal endothelial marker; PEM;
pan-endothelial marker; polycystic kidney disease; psoriasis;
diabetic retinopathy; rheumatoid arthritis; tumour anglogenesis;
necanglogenesis; immune response; cytostatic; antidiabetic;
ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 637; DB 5; Length 161;
Pred. No. 1.6e-54;
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Disclosure, Page, 56pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 161 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
                                                                                                                                                                                                                                                                                                                                                             49 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKGHVLFGTVGVPEHTYRSRTN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disease; arthritide; gene expression analysis; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antigout; antiinflammatory; dermatological; immunomodulatory; lugus; ankylosing spondylitis; Fibrositis; fibromyalgis; osteoarthritis; gout; juvenile rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                             109 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 FISKYHMKVLYLSAFISKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139
                          The present invention relates to a novel method for the isolation of endothelial cells (ECB), and the identification of genes expressed in normal and tumour ECB. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal marker (TEM), and pan-endothelial marker (PEM) genes are identified in human ECB. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriaais. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour andiogenesis, for for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
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                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                          Length 161;
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                                                                                                                                                                                                                                                                                          Score 637; DB 6; I
Pred. No. 1.6e-54;
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100.0%; Pred. No....
0; Mismatches
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Disclosure; Page 206-207; 374pp; English.
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                                                                                                                                                                                                                                                                                    Query Match 67.5
Best Local Similarity 100.
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thorton SL;
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                                                                                                                                                                                                                                                        Sequence 161 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP65208;
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The invention fracters to a move, method comprises obtaining a teneinmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA comparison signature of the mRNA, and using the mRNA comparison signature of the mRNA, and using that gene expression signature of the mRNA, and using that compression signature of the manual disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention of further comprises: a treatment of rheumatoid arthritis; identification of coher than a mouse; diagnosis of rheumatoid arthritis; in a mammal of array or gene chip, specific for rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; accening the confidenced arthritis; and reducing the symptoms associated with collagentinduced arthritis; and reducing attendation of the present invention are useful for antigout, antititis, lupus, ankylosing spondylitis, fibrositis, themmatoid arthritis, lupus, ankylosing spondylitis, fibrositis, inchesses caused by an infectious agent. This sequence reparement of immune disease or arthritides, manualy sequence is not shown in the specification. It has been supplied in an electronic format from
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invention relates to a novel method for diagnosing and analysing
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Pred. No. 7.9e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1, Mismatches
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N-PSDB; ADZ13571.
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                                                                                                                        associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer drug candidate and monitoring the effect of the anticancer drug candidate and monitoring the offer of the anticancer drug candidate of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test cell sample and for screening for a bloactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a human CAP of the invention. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 FTSKYNMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139
                                                                                                                                                                                                                                                                                                                                                                                                                 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                        20 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 79
                                                                                                                The invention relates to cancer-associated proteins (CAP) and the cancer
                                                 Novel human cancer associated protein encoded within open reading frame of cancer associated gene, useful as targets for diagnosing cancer.
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                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                       Claim 18; SEQ ID NO 20; 182pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer-associated protein #329.
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             WPI; 2004-499109/47.
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                                                                                                                                                                                                                                                                                                                                       Sequence 161 AA;
                         N-PSDB; ABD33081
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The invention relates to a nucleic acid array for detecting a cancer associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing animal antibody and a carrier, a method of screening for anticancer activity, a method of tetecting a CA nucleic acid, a method of flagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA nucleic acids are useful for detecting CA nucleic acids are not an individual which involves contacting cells from the individual which involves contacting cells from the individual with the antibody and detecting a complex of a CA protein from the cancer cells and the antibody and detecting a complex of a CA protein from the cancer cells and the antibody where the detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual. The invention at therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA gene in a cell. This sequence represents a human cancer-associated protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 OKVISLIACLVDOSLRLDCRHENTSSSPIQYEFSLIRETKGHVLFGTVGVPEHTYRSRIN 108
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Nucleic acid array useful for detecting cancer associated nucleic acid, comprises two or more nucleic acid probes.
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                                                                                                                          Disclosure; SEQ ID NO 1092; 198pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 121; Conservative
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Human cancer associated protein sequence SEQ ID NO:1384.
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               07-APR-2005.
                                                                                                                              Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention.
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AAB43939
ID AAB43
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                                                                                                                                                                              The invention relates to a nucleic acid array for detecting a cancer associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunicing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against the antipod and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA nucleic acids are useful for detecting CA absence of absence of absence or absence of an individual which involves contacting cells and a calls in an individual which involves contacting cells
                                                                                                                                                                                                                                                                                                                                                                                                    from the individual with the antibody and detecting a complex of a CA protein from the cancer cells and the antibody, where the detection of the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA gene in a cell. This sequence represents a human cancer-associated protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKGHVLFGTVGVPEHTYRSRTN 108
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                                                                                                               Nucleic acid array useful for detecting cancer associated nucleic acid, comprises two or more nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKVTSLTACLVDQSLRLDCRHENTSSSP1QYEFSLTRETKKHVLFGTVGVPEHTYRSRTN
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Pred. No. 7.9e-54;
1; Mismatches 0;
                                                                                                                                                       Disclosure; SEQ ID NO 1094; 198pp; English.
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99.2%;
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                                          Morris DW, Malandro MS;
             (CHIR ) CHIRON CORP.
                                                                      WPI; 2005-273395/28
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                                                                                     N-PSDB; ADZ13573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 161 AA;
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The invention relates to a nucleic acid array for detecting a cancer associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against fragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the cartion or its antigen binding fragment, a composition comprising the cancer cells antibody and a carrier, a method of fargmosting cancer, a method of treating acancer and a method of inhibiting expression of a CA nucleic acid, a method of diagnosing cancer, a method of treating and a cell. The CA nucleic acids are useful for detecting CA nucleic acids are useful for detecting cancer cells in an individual which involves contacting cancer cells in an individual which involves contacting cells from the individual. The composition is useful for inhibiting growth of cancer cells in an individual. The invention is also useful for diagnosing calls in an individual. The invention is also useful for diagnosing calls in an individual. The invention is also useful for diagnosing calls in an individual. This sequence represents a human cancer-associated protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid array useful for detecting cancer associated nucleic acid, comprises two or more nucleic acid probes.
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Pred. No. 7.9e-54;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, SEQ ID NO 1090; 198pp; English.
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23-SEP-2004; 2004WO-US031617.
                                                                                     23-SEP-2003; 2003US-00669920.
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                                                                                                                                                                                                                                                                         Malandro MS;
                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-273395/28.
N-PSDB; ADZ13569.
                                                                                                                                                                               (CHIR ) CHIRON CORP.
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us-10-611-655-10.rag

RESULT 12

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Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiaschmatic; antinheumatic; antiarchritic; antiviral; antilnflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; cogulatar; noctropic; vasocropic; antiparatic, antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; haematopoietic cell disorder; autoimmune disorder; haemostatic; cardiovascular disease; organ rejection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 2053-2054; 2352pp; English.
                                                                                                                                                                                                                08-MAR-2000; 2000WO-US005882.
                                                                                                                                                                                                                                         99US-0124270P.
                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present invention
                                                                                                                                                                                                                                                                                          Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                    2000-587533/55.
                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC78148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 165 AA;
                                                                                                                                                               WO200055350-A1.
                                                                                                                                                                                                                                         12-MAR-1999;
                                                                                                                                         Homo sapiens
                                                                                                                                                                                       21-SEP-2000
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AAC77607 to AAC7848 encode the human cancer associated proteins given in AAB43398 to AAB4429. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antialery; immunomodulator; antidiabetic; antiasthmatic; antialery; antiarthritic; antinflammatory; antithyroid; antialery; antibacterial; antiviral; correctoric; assortopic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or meliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides can be used for preventing, treating or the present invention may be used to treat immune disorders by activating or thibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate corrected or viral infections. The peptides, nucleotides, antibodies, bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be used to used in the exemplification of the account and antagonists may be used to be used in the exemplification of QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108 PTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168 24 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKKVLFGTVGVPEHTYRSRTN 83 Gaps ö Length 165; 0; Indels Score 630; DB 3; Pred. No. 8.2e-54; 1; Mismatches 0; 66.7**%**; 99.2**%**; Conservative Query Match Best Local Similarity TS 170 121; 109 49 169 Best Loca Matches 셤 δ 유 8

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cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. Additionally and Additionally represent C carcinomas and cancers. Additioal cancer associated Ps. By inserting the involving the colorectal carcinomas and cancers. Additioal cancer associated by the series the proteins. N and P carcinomas and cancers associated of the sequence used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FISKYHMKVLYLSAFISKDEGIYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                    Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 630; DB 4; Length 165;
Pred. No. 8.2e-54;
1; Mismatches 0; Indels
                                                                                                                                Human colon cancer antigen protein SEQ ID NO:4614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 6411-6412; 9803pp; English.
                                                                                                                                                                                         colorectal carcinoma; chromosome 11.
                AAG73850 standard; protein; 165 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM, Barash SC, Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.7%;
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                                                                                                                                                                                                                                                                                                                                                   28-SEP-2000; 2000WO-US026524.
                                                                                                                                                                                                                                                                                                                                                                                            99US-0157137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                         03-SBP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 99.2 Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAH33281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TS 170
                                                                                                                                                                                                                                                                      WO200122920-A2.
                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                            29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                              03-NOV-1999;
                                                                                                                                                                                                                                                                                                           05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
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                                                    AAG73850;
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AAG73850
                                                      셤
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(revised)
(first entry)

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AAY31789 standard; protein; 368 AA.
                                                                       17-OCT-2003
06-DEC-1999
                                              AAY31789;
                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                     Peptide
RESULT 14
            AAY31789
                                              원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide. The polypeptide comprises an immunoglobulin-like domain containing scaffold with two or more solvent exposed loops containing a different complementarity-determining region (CDR) from a parent antibody inserted into each of the loops and exhibiting selective binding activity coward a ligand bound by the parent antibody. The invention further comprises a chimeric Thyox binding polypeptide, comprising one or more altered immunoglobulin-like domain loop regions of a Thyox family polypeptide or at least one immunoglobulin-like domain containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scaffold derived from a Thyox family polypeptide, and a heterologous binding polypeptide exhibiting selective binding activity toward a non-Thyox ligand; and a nucleic acid encoding the non-immunoglobulin or Thyox binding polypeptide above. The chimeric non-immunoglobulin binding polypeptide is useful for producing non-immunoglobulin binding polypeptides having selective binding activity toward a predetermined molecule. This sequence represents a human Thy-1 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 FISKYHMKVLYLSAFISKDEGTYTCALHHSGHSPPILLSSQNVTVLRDKLVKCEGISLLAQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPI-SSQNVTVLRDKLVKCEGISLLAQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEESLITRETKKHVLFGTVGVPEHTYRSRTN 79
                                                                                                                                                                                                                                                                                                                                                      New chimeric non-immunoglobulin binding polypeptide comprises immunoglobulin-like domain containing scaffold and exhibits selective binding activity, for producing non-immunoglobulin binding polypeptides with selective binding activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEPSLTRETKKHVLFGTVGVPEHTYRSRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to a novel chimeric non-immunoglobulin binding
                                                                                                                                 non-immunoglobulin binding polypeptide; selective binding; Thy-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.4e-52;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 617.5;
                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 1; 45pp; English.
                                 ADW10183 standard; protein; 162 AA.
                                                                                                                                                                                                                                30-JUN-2003; 2003US-00611655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.4%;
                                                                                                                                                                                                                                                        30-JUN-2003; 2003US-00611655
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 65.4
Best Local Similarity 98.4
Matches 121; Conservative
                                                                                                          Human Thy-1 protein.
                                                                                                                                                                                                                                                                                                                               WPI; 2005-047648/05.
                                                                                                                                                                                                                                                                                 (EVAN/) EVANS G A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTS 142
                                                                                                                                                                                 US2004266993-A1
                                                                                                                                                          Homo sapiens
                                                                                 24-MAR-2005
                                                                                                                                                                                                         30-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nvention
                                                         ADW10183;
                                                                                                                                                                                                                                                                                                       Evans GA;
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The present sequence represents a fusion protein, the mature region of which is claimed, comprising the human Thy-1 extracellular region (see AAY31787) and the constant region (hinge, CH2, CH3) of human 19G1. A claimed method for inhibiting anglogenesis in a mammal comprises administering a compound that inhibits Thy-1 associated proliferation of an endothelial cell. The compound is preferably the extracellular region of rat or human Thy-1. The method is used in the treatment of a mammal having a tumour (e.g. by reducing vascularisation), atheroselerosis or rheumatoid arthritis, the lesions of which may be associated with covascularisation (all claimed). Another claimed method for inhibiting angiogenesis involves administering a Thy-1 antisense nucleic acid or a Thy-1 specific antibody linked to a cytocoxic agent. A method for promoting angiogenesis involves administering a compound that increases promoting angiogenesis involves administering a compound that increases promoting angiogenesis involves administering a compound that increases comprising the Thy-1 extracellular fragment and the constant region of an immunoglobulin. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                         18. .368
/note= "Thy-1-Ig fusion, specifically claimed in Claim 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 79
                                                                 Thy-1; human; IgG; angiogenesis; cancer; tumour; rheumatoid arthritis; atherosclerosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 8.2e-51;
2; Mismatches 9; Indels
Human Thy-1-human IgG constant region fusion protein.

    19
    note= "Thy-1 signal peptide"

                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 46-47; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US005256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00077524
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Best Local Similarity 91.33
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARD ) HARVARD COLLEGE. (HABE/) HABER C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-561618/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haber E, Shaw S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX87980
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                                                                                                                                                                               Homo sapiens
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-1999;
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Search completed: December 6, 2005, 10:36:50 Job time : 165.348 secs

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The present sequence represents the extracellular region of human Thy-1, a protein expressed by vascular endothelial cells during angiogenesis. A claimed method for inhibiting angiogenesis in a mammal comprises and comprises and compound that inhibiting the associated proliferation of an endothelial cell. This compound is preferably the extracellular region of thuman or rat (see AXY21786) Thy-1. The method is used in the treatment of a mammal having a tumour (e.g. by reducing vascularisation), atherosclerosis and rheumatoid arthritis, the lesions of which may be associated with neovascularisation (all claimed). Another claimed method for inhibiting angiogenesis involves administering a Thy-1 antisense nucleic acid or a Thy1-specific antibody linked to a cytotoxic agent. A method for promoting angiogenesis involves administering a compound that method for promoting angiogenesis involves administering a compound that comprising the Thy-1 extracellular fragment and the constant processor in immunoglobulin (see AXY31788)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKGGVLFGTVGVPEHTYRSRTN 108
80 PISKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLADKLVKCEGADLSSRP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGADL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                        Thy-1; human; angiogenesis; cancer; tumour; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.6%; Score 600; DB 2; Length 119; 98.3%; Pred. No. 4.9e-51; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                              AAY31787 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                     Human Thy-1 extracellular fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 4; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US005256.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jain MK,
                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                            atherosclerosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HARD ) HARVARD COLLEGE. (HABE/) HABER C.
                                                       169 TSHHHHH 175
                                                                                        140 KSSDKTH 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-561618/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shaw S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                  06-DEC-1999
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                                                                                                                                                                                                               AAY31787;
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December 6, 2005, 10:37:02 ; Search time 4.64111 Seconds (without alignments) 114.521 Million cell updates/sec
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605
1 QVSRGQKVTSLTACLVDQSL......VLRDKLVKCEGVYYRYYFDY 111
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1: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

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6: /cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

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8: /cgn2 6/ptodata/1/pubpaa/US11 NEW PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/US11 NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26661 seqs, 4788334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Description	
7	118	19.5	121	7	US-11-108-135-28	Sequence 28, Appl	
8	115	19.0	122	9	US-10-932-334-73	73,	
m	109	18.0	120	9	US-10-932-334-71	71,	
4	109	18.0	120	9	US-10-932-334-72	Sequence 72, Appl	
S	101	16.7	248	9	US-10-512-184-36	36,	
9	101	16.7	615	9	US-10-512-184-50	20,	
7	100	16.5	121	^	US-11-108-135-24	Sequence 24, Appl	
8	100	16.5	123	9	US-10-932-334-87	87,	
a	100	16.5	123	9	US-10-932-334-88	88	
10	100	16.5	123	9	US-10-932-334-92	8	
11	100	16.5	124	9	US-10-932-334-7	Sequence 7, Appli	
12	100	16.5	124	ø	US-10-932-334-13	13	
13	100	16.5	124	9	US-10-932-334-70	2	
14	100	16.5	143	ø	US-10-932-334-52	25	
15	66	16.4	98	ø	US-10-932-334-57		
16	97.5	16.1	248	~	US-11-054-515-2088		
17	97	16.0	247	7	US-11-054-515-2103	Sequence 2103, Ap	
18	96	15.9	120	9	US-10-932-334-74	Sequence 74, Appl	
19	92	15.2	120	7	US-11-173-071-2	Sequence 2, Appli	
20	92	15.2	121	9	US-10-507-662-25	25,	
21	92	15.2	121	9	-10-507-	Sequence 26, Appl	
22	90	14.9	138	7		Sequence 3, Appli	
23	87	14.4	255	7	-11-054-	_	
24	87	14.4	257	7	<del>-</del>	1514	
25	98	14.2	115	9	US-10-932-334-80	Sequence 80, Appl	

Sequence 21, Appl Sequence 1919, Ap	Sequence 2084, Ap	Sequence 1995, Ap	Sequence 32, Appl	Sequence 57, Appl	Sequence 21, Appl	Sequence 75, Appl	47,	Sequence 50, Appl	Seguence 35, Appl	Sequence 77, Appl	Sequence 79, Appl	Sequence 81, Appl	Sequence 12, Appl	Sequence 14, Appl	Sequence 29, Appl	Sequence 1418, Ap	Seguence 1672, Ap	Sequence 30, Appl
US-10-502-145-21 US-11-054-515-1919	US-11-054-515-2084	US-11-054-515-1995	US-10-507-662-32	US-11-096-074-57	US-11-084-717-21	US-10-932-334-75	US-11-065-943-47	US-11-096-074-50	US-10-507-662-35	US-10-932-334-77	US-10-932-334-79	US-10-932-334-81	US-11-173-071-12	US-11-173-071-14	US-10-839-799-29	US-11-054-515-1418	US-11-054-515-1672	US-10-507-662-30
9 1	7	7	9	7	7	9	7	7	9	9	9	9	7	7	9	7	7	9
121	242	248	118	125	247	118	114	116	118	120	120	121	128	128	136	253	253	118
14.2	14.0	14.0	13.9	13.9	13.8	13.7	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.4
986	82	84.5	84	84	83.5	83	82.5	82	85	82	82	82	82	82	82	82	85	81
26	78	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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Best Local Similarity 33.3%; Pred. No. 9.2e-07;
Matches 29; Conservative 14; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: Mouse 2B6 heavy chain variable region US-11-108-135-28
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RESULT 2 US-10-932-334-73

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
19.0%; Score 115; DB 6; Length 122;
Best Local Similarity 28.7%; Pred. No. 2e-06;
Matches 25; Conservative 19; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.0%; Score 109; DB 6; Length 120; 31.7%; Pred. No. 8.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 --- DKP-SSTAYMQLSSLTSEDSAVYYCARYDYYGSSYFDY 109
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Sequence 71, Application US/10932334

Publication No. US20050249728A1

GENERAL INFORMATION:

TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY

FILE REFERENCE: A8689

CURRENT APPLICATION NUMBER: US/10/932,334

CURRENT PILING DATE: 2004-09-02

PRIOR FILING DATE: 2003-12-08

PRIOR FILING DATE: 2003-12-08

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PATENTION NOWER: 10,170,390

HOWER OF SEQ ID NOS: 96

SEQ ID NO 71

LENGTH: 120
                                                              APPLICANT: Immunoden, Inc.
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILLE REFERENCE: A8689
CURRENT APPLICATION NUMBER: US/10/932,334
CURRENT FILING DATE: 2004-09-02
PRIOR APPLICATION NUMBER: US/10/729,441
PRIOR PILING DATE: 2003-12-08
PRIOR PILING DATE: 2003-12-08
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn version 3.2
LENGTH: 122
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                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: synthetic antibody structure
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Matches 32; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 SGHSPPISSQNVTVLRDKLVKCEGVYY 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 SSSTAYMQLSSLTSEDSAVYYCASLYY 101
Sequence 73, Application US/10932334
Publication No. US20050249728A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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RESULT

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Sequence 36, Application US/10512184

Publication No. US20050244901A1

GENERAL INFORMATION:

APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.

TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: resistance against fungi

FILE REFERENCE: 3581.01US01

CURRENT APPLICATION NUMBER: US/10/512,184

CURRENT FILING DATE: 2004-10-22

NUMBER OF SEQ ID NOS: 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.0%; Score 109; DB 6; Length 120; 31.7%; Pred. No. 8.9e-06; Live 11; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 SGHSPPISSONVTVLRDKLVKCEGVYY--RY-----YFDY 111
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                                                                                                        TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY FILLS OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY FILLS OF INVENTION ANTI-IGF-I RECEPTOR ANTIBODY CURRENT PAPLICATION NUMBER: US/10/932,334
CURRENT FILING DATE: 2004-09-02
PRIOR APPLICATION NUMBER: US/10/729,441
PRIOR PILING DATE: 2003-06-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFFWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-72
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US-10-932-334-72
; Sequence 72, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 32; Conserv
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Matches 27; Conserv
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US-10-512-184-36
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LENGTH: 248
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LENGTH: 120
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19 SLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTIDPADSYTSYNONFKDEGTYTCALHH 78
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73
                                           SLRLDCRHENTSSSNYWMFSLTRETKKHVLFGTIDPADSYTSYNONFKDEGTYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAPLICATI: ImmunoGen, Inc.
TITLE OF INVENTION: ANTI-IGP-I RECEPTOR ANTIBODY
FILE REFERENCE: A8699
CURRENT APPLICATION NUMBER: US/10/932,334
CURRENT FILING DATE: 2004-09-02
PRIOR APPLICATION NUMBER: US/10/729,441
PRIOR APPLICATION NUMBER: US/10/729,441
PRIOR PILING DATE: 2003-12-08
PRIOR PLING DATE: 2003-614
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFERENCE: A8689
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CURRENT FILING DATE: 2004-09-02
PRIOR APPLICATION NUMBER: US/10/729,441
PRIOR PILING DATE: 2003-12-08
PRIOR PILING DATE: 2003-12-08
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin version 3.2
SEQ ID NO 88
LENGTH: 123
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; Sequence 88, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  ; Sequence 87, Application US/10932334; Publication No. US20050249728A1; GENERAL INFORMATION:
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Best Local Similarity 26.0%
Marches 27; Conservative
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Sequence 24, Application US/11108135

Sequence 24, Application US/11108135

Publication No. US20050260213A1

GENERAL INFORMATION:

APPLICANT: Roanig, Scott

APPLICANT: Stavenhagen, Joeffrey

APPLICANT: Stavenhagen, Joeffrey

APPLICANT: Rankin, Christopher

TITLE OF INVENTION: FC-gamma-RIIB-specific antibodies and methods of use thereof

FILE REFERENCE: 11183-014-999

CURRENT APPLICATION NUMBER: US/11/108,135

CURRENT APPLICATION NUMBER: US 60/562,804

PRIOR PILING DATE: 2004-04-16

PRIOR PLING DATE: 2004-04-16

PRIOR PLING DATE: 2004-06-21

PRIOR PLING DATE: 2004-06-21

PRIOR APPLICATION NUMBER: US 60/582,045

PRIOR PLING DATE: 2005-02-18

PRIOR PLING DATE: 2005-02-18

PRIOR PLING DATE: 2005-02-18

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 121

FURNEL FOR THE CONTROL T
                        Sequence 50, Application US/10512184

Publication No. US20050244901A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies, recombinant TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease TITLE OF INVENTION: resistance against fungi FILE REFERENCE: 3581.01US01
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: Description of Artificial Sequence: fusion protein of Trificial Sequence: fusion protein of OTHER INFORMATION: comprising the leader peptide - chitinase - linker comprising the leader peptide - chitinase - linker comprising the leader peptide - chitinase - linker compress of the com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 29.0%; Pred. No. 0.00046;
Matches 27; Conservative 15; Mismatches 49,
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ORGANISM: Artificial Sequence
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RESULT 13
US-10-932-334-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
16.5%; Score 100; DB 6; Length 123;
Best Local Similarity 26.0%; Pred. No. 9e-05;
Matches 27; Conservative 17; Mismatches 40; Indels 20; Gaps
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16.5%; Score 100; DB 6; Length 124;
Best Local Similarity 26.0%; Pred. No. 9.1e-05;
Matches 27; Conservative 17; Mismatches 40; Indels
                                                 79 SGHSPPISSQNVTVLRDKLVKCEGVYY-------RYYFD 110
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Publication No. US20050249728A1

GENERAL INFORMATION:

APPLICANT: ImmunoGen, Inc.

TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REPERENCE: A669

CURRENT PILING DATE: 2004-09-02

PRIOR APPLICATION NUMBER: US/10/932,334

CURRENT FILING DATE: 2003-12-08

PRIOR APPLICATION NUMBER: 10/170,390

PRIOR PILING DATE: 2003-12-08

PRIOR PILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PATENTIN Version 3.2

SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY FILE REFERENCE: A8689
FILE REFERENCE: A8689
CURRENT APPLICATION NUMBER: US/10/932,334
CURRENT FILING DATE: 2004-09-02
PRIOR APPLICATION NUMBER: US/10/729,441
PRIOR PILING DATE: 2003-12-08
PRIOR FILING DATE: 2003-12-08
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PATENTIN NOS: 96
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 92
LEAST AREA OF SECTION 
79 SCHSPPISSQNVTVLRDKLVKCEGVYY--
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                                                                                                                                                                                                                                                                     Sequence 92, Application US/10932334 Publication No. US20050249728A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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19 SLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. SVKLSCKASGYTFTSYWMHWVKQRPQGLEWIGEINPSNGRTNYNQKFQGKATLTV--- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.5%; Score 100; DB 6; Length 124; 26.0%; Pred. No. 9.1e-05; tive 17; Mismatches 40; Indels
  -RYYFD 110
                                 79 SGHSPPISSQNVTVLRDKLVKCEGVYY-------RYYFD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---- DKSSSTAYMQLSSLTSEDSAVYYFARGRPDYYGSSKWYFD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: humanized heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 70. Application US/10912334

Publication No. US20050249728A1

GENERAL INFORMATION:

APPLICART: ImmunoGen, Inc.

TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFRENCE: A8689

CURRENT FILING DATE: 2004-09-02

PRIOR PILING DATE: 2003-12-08

PRIOR FILING DATE: 2003-12-08

PRIOR FILING DATE: 2002-6-14

NUMBER OF SEQ ID NOS: 96

SOFTWARE: Patentin version 3.2

SEQ ID NO 70
                                                                                                                                                                                                                                                              APPLICANT: ImmunoGen, Inc.
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFERENCE: 40669
CURRENT APPLICATION NUMBER: US/10/932,334
CURRENT FILING DATE: 2004-09-02
PRIOR APPLICATION NUMBER: US/10/729,441
PRIOR PILING DATE: 2003-12-08
PRIOR APPLICATION NUMBER: 10/170,390
PRIOR FILING DATE: 2002-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-70
79 SGHSPPISSONVTVLRDKLVKCEGVYY-
                                                                                                                                                        US-10-932-334-13; Sequence 13, Application US/10932334; Publication No. US20050249728A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 96
SOFTWARB: PatentIn version 3.2
SEQ ID NO 124
LENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27; Conservative
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Best Local Similarity
Matches 27; Conserva
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Best Local Similarity
Matches 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 SVKLSCKASGYTFTSYMMHWVKQRPGGGEWIGEINPSNGRTNYNEKFKRKATLTV---- 91
17 SVXLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEINPSNGRTNYNEKFKRKATLTV---- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 SLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTIDPADSYTSYNONFKDEGTYT 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.4%; Score 99; DB 6; Length 98; Best Local Similarity 32.7%; Pred. No. 8.9e-05; Matches 18; Conservative 14; Mismatches 23; Indels
                                                79 SGHSPPISSQNVTVLRDKLVKCEGVYY ------RYYFD 110
                                                                         79 SGHSPPISSONVTVLRDKLVKCEGVYY-------RYYFD 110
                                                                                                                                                                                       Sequence 52, Application US/10932334

Publication No. US20650249728A1

GENERAL INFORMATION:

APPLICANT: ImmunoGen, Inc.

TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY

FILE REFERENCE: A8689

CURRENT APPLICATION WUMBER: US/10/932,334

CURRENT APPLICATION WUMBER: US/10/729,441

PRIOR APPLICATION WUMBER: 10/1729,441

PRIOR FILING DATE: 2003-12-08

PRIOR FILING DATE: 2003-12-08

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 52

LENGTH: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5.2.4.5.4

Publication No. US20050249728A1

Sequence 5.0.4.0.20050249728A1

SEQUENCE INFORMATION:

APPLICANT: ImmunoGen, Inc.;

TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY

FILE REFERENCE: A8689

CURRENT APPLICATION NUMBER: US/10/932,334

CURRENT FILING DATE: 2004-09-02

PRIOR APPLICATION NUMBER: 10/10/390

PRIOR APPLICATION NUMBER: 10/170,390

PRIOR APPLICATION NUMBER: 10/170,390

PRIOR APPLICATION NUMBER: 10/170,390

SETOR FILING DATE: 2003-12-08

SEQ ID NOS: 96

SOFTWARE: Patentin version 3.2

SEQ ID NO 57

LENGTH: 98
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CRGANISM: Mus musculus
US-10-932-334-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-932-334-52
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Search completed: December 6, 2005, 10:48:05 Job time : 5.64111 secs

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6, 2005, 10:32:13; Search time 25.9129 Seconds (without alignments) 354.148 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                           1 QVSRGQKVTSLTACLVDQSL.....VLRDKLVKCEGVYYRYYFDY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/laa/5_COMB.pep:*
/cgn2_6/ptodata/1/laa/6_COMB.pep:*
/cgn2_6/ptodata/1/laa/H_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/RE_COMB.pep:*
/cgn2_6/ptodata/1/laa/RE_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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605
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Perfect score:
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, Description	Sequence 11168, A	Sequence 4247, Ap	Sequence 12, Appl	Sequence 12, Appl	12,	Sequence 15, Appl	15,	17,	17,	17,	6, 2	59	118,	118,	14,	62,	30,	œ	Sequence 2, Appli	Sequence 2, Appli	œ	Sequence 8, Appli	Sequence 59, Appl	Sequence 17, Appl	Sequence 63, Appl	16,	Sequence 61, Appl
O.	US-09-949-016-11168	US-09-513-999C-4247	US-10-092-246-12	US-10-096-246A-12	US-08-553-497A-12	US-09-065-059-15	US-08-913-555-15	US-08-672-345C-17	US-09-214-095D-17	US-09-940-727B-17	US-08-767-128-6	US-08-273-146-59	US-09-214-095D-118	US-09-940-727B-118	US-08-881-037-14	US-08-881-037-62	US-09-069-628-30	US-08-553-497A-8	US-08-800-198-2	US-09-296-595-2	US-08-800-198-8	US-09-296-595-8	US-08-881-037-59	US-08-881-037-17	US-08-881-037-63	US-08-881-037-16	US-08-881-037-61
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% Query Match Length DB	161	105	120	120	119	117	117	116	116	116	119	113	113	113	111	119	146	119	119	119	240	240	98	111	119	111	119
A Query Match	70.1	40.1	20.8	20.8	20.7	20.7	20.7	20.6	20.6	20.6	20.4	20.3	20.3	20.3	20.2	20.2	20.2	20.1	20.1	20.1	20.1	20.1	20.0	19.9	19.9	19.8	19.8
Score	424	242.5	126	126	125.5	125	125	124.5	124.5	124.5	123.5	123	123	123	122.5	122.5	122.5	121.5	121.5	121.5	121.5	121.5	121	120.5	120.5	119.5	119.5
Result No.	н	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27

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Sequence 11168

Sequence 11168. Application US/09949016

Sequence 11168. Application US/09949016

Sequence 11168. Application US/09949016

Sequence 11168. Application US/09949016

SERVERL INVENTION: DELYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-0-04-1, 755

PRIOR PELICATION NUMBER: 60/241, 756

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

SOUTHWARE OF SEQ ID NOS: 207012

SOUTHWARE PRESEDE FOR WINDOWS VERSION 4.0
                                                                        15, Appl
60, Appl
4, Appli
4, Appli
4, Appli
4, Appli
12, Appli
12, Appli
12, Appli
12, Appli
11, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-09-513-999C-4247
; Sequence 4247, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Glordano, J.Y.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.; Patent No. 6783991
; PILE REFERENCE: 59. US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTID-PADSY
                                                          Sequence 9, 7
Sequence 15,
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Sequence 11,
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Sequence 16,
                     Sequence
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70.1%; Score 424; DB 2; Length 161;
Best Local Similarity 73.9%; Pred. No. 1.1e-40;
Matches 88; Conservative 3; Mismatches 12; Indels 1
US-09-406-532-2
US-09-726-219A-226
US-09-196-522-226
US-09-196-522-226
US-08-881-037-15
US-08-891-037-60
US-08-891-037-60
US-08-891-1037-60
US-09-125-107-4
US-09-125-107-4
US-09-526-738A-4
US-09-526-738A-4
US-09-526-738A-1
US-08-621-751A-12
US-08-621-751A-12
US-08-621-751A-12
US-08-63-638-8-11
US-08-465-4738-11
                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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US-09-949-016-11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 11168
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Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
Virus (VEE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 SVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEIDPSDSYTYYNQKFKGKATLT--VDK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SINGLE-CHAIN FVS AND ANTI-EGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 SGHSPPISSQNVTVLRDKLVKCEGVYY--RYYFDY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 20.8%; Score 126; DB 2; Best Local Similarity 32.6%; Pred. No. 9.4e-07; Matches 31; Conservative 16; Mismatches 44
   TITLE OF INVENTION: Monoclonal ScFV Antibody
TITLE OF INVENTION: Virus (VEE)
FILE REFERENCE: NEL-0007
CURRENT APPLICATION UNMBER: US/10/096,246A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.2
SEQ ID NO 12
LENGTH: 120
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08553497A Patent No. 5844093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: KETTLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSOW, DETLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-EGFR ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADAN, JAUME
MITJANS, FRANSESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS ADDRESS ADDRESSEE: MILLEN, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: mouse US-10-096-246A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SD
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: V. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Sequence 12, Application US/10092246

Patent No. 6501314

GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: Alvi, Azhar E
APPLICANT: Magata, Leslie
APPLICANT: Magata, Leslie
APPLICANT: Nagata, Leslie
APPLICANT: Nagata, Leslie
APPLICANT: Serv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
FILE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/092,246
CURRENT APPLICATION NUMBER: US/10/092,246
CURRENT PILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOPTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
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| Sequence 12, Application US/10096246A
| Patent No. 68187H2
| GENERAL INFORMATION:
| APPLICANT: Fulton, R. Elaine
| APPLICANT: Nagata, Lealie
| APPLICANT: APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTID-PADSY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 SLRLDCRHENTSSSNYWMFFSLTRETKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 40.1%; Score 242.5; DB 2; Best Local Similarity 62.5%; Pred. No. 3.6e-20; Matches 55; Conservative 6; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 SSSTAYMOFSSLTSEDSAVYYCARRYYGSRVSMDY 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 SGHSPPISSQNVTVLRDKLVKCEGVYY--RYYPDY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 RSRTNFTSKYNMKVLYLSASLARTRALH 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 ---TSYNQNFKDEGTY-----TCALH 77
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                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SIGNAL
LOCATION: -19.-1
JOTHER INFORMATION: score 11.7
JOTHER INFORMATION: seq IALLITVLQVSRG/QK
US-09-513-999C-4247
           CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SEQ ID NO 4247
LENGTH: 105
                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -10-092-246-12
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LENGTH: 120
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16 SVKMSCKASGYTFTTYWMHWVKQRPGQGLEWIGYINPSSGYTEYNQKFKDKATLT----

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                                                                                                                                                                                                                                                                                                                                               17 SVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEIDPSDSYTNYNQKFKGKATLT--VDK 74
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Indels 14;
                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                    Length 119;
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                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: SEINO, Ken-ichiro
APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: YAGITA, Hideo
APPLICANT: OKUMUNA, Ko
APPLICANT: OKUMUNA, Ko
APPLICANT: NAKATA, MOLONA
ITTLE OF INTENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESSEE: MCDETMOCK, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPES Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
                                                                                                                                                                                                               Query Match
20.7%; Score 123.3; we 1,
Best Local Similarity 31.9%; Pred. No. 1.1e-06;
Matches 30; Conservative 18; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                      79 SGHSPPISSQNVTVLRDKLVKC-EGVYYRYYFDY 111
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-518-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09065059 Patent No. 6068841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELERAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
                    TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
  703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide US-09-065-059-15
                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-553-497A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
  TELEPHONE:
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GENERAL INFORMATION:
APPLICANT: KAYAGAKI, No. 6946255uhiko
APPLICANT: YAGITA, Kideo
APPLICANT: OXUMURA, Kideo
APPLICANT: OXUMURA, Motomi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: REACTING WITH FAS LIGAND AND PRODUCTION PROCESS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 SLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTIDPADSYTSYNONFKDEGTYTCALHH 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
CORFATION SYSTEM: PC-DOS/NS-DOS
CORFARIE: Patentin Release #1.0, Version #1.30
CORFATION NUMBER: US/08/913,555
FILING DATE: 19-SEP-1997
CLASSIFICATION NUMBER: 42,366
REGISTRATION NUMBER: 42,366
REFERENCE/DOCKET NUMBER: 50356-150
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 594668

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 SGHSPPISSQNVTVLRDKLVKCEGVYY-----RYYFDY 111
79 SGHSPPISSONVTVLRDKLVKCEGVYY-----RYYFDY 111
                                                      ---ADKSSSTAYMQLISLTSEDSAVYYCARRGNYYYFDY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: McDermott, Will & Emery
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                  . Sequence 15, Application US/08913555; Patent No. 6946255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-756-8699
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.7% Best Local Similarity 31.3% Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-672-345C-17
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Cooper and Dunham LLP

ADDRESSEE:

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USA
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US-09-940-727B-17
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-08-767-128-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 SLRLDCRHENTSSSNYWMHPSLTRETKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 SLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTIDPADSYTSYNONFKDEGTYTCALHH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 SVKMSCKASGYTFIDHWMHWVKQRPGGGLEWIGTIDLSDIYYGYNQNFKGRATLI--LDE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 20.6%; Score 124.5; DB 1; Length Best Local Similarity 32.3%; Pred. No. 1.3e-06; Matches 30; Conservative 18; Mismatches 42; Indels
                                     STATE: New IOLA.

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTON PATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 0575/51400
TELECOMMUTICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPAX: 212-391-0525
INFORMATION FOR SED ID NO: 17:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SED ID NO: 17:
SEQUENCE CHARACTERISTICS:
INFORMATION CORE OF INFORMATION:
TELEPAX: 212-391-0525
INFORMATION COR SED ID NO: 17:
SEQUENCE CHARACTERISTICS:
INFORMATION COR SED ID NO: 17:
SEQUENCE CHARACTERISTICS:
INFORMATION CORE OF SEQUENCE
TYPE: amino acid
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE: protein
US-08-672-345C-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-214-095D-17
i Sequence 17, Application US/09214095D
i Patent No. 6280987
i GENERAL INFORMATION:
i APPLICANT: Landry, Donald
i TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/214,095D
i CURRENT FILING DATE: 1999-07-19
i NUMBER OF SEQ ID NOS: 121
i SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 SGHSPPISSQNVTVLRDKLVKCEGVYYRYFDY 111
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STREET: 1185 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-17
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LENGTH: 116
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SEGURATION: LANGE AND LIGHT AND STATE AND SEGURATED SEGURATION SEG
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MOLECULE TYPE: protein US-08-273-146-59
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US-09-214-095D-118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 LRLDCRHENTSSSNYMMHFSLTRETKKHVLFGTIDPADSYTSYNONFKDEGTYTCALHHS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    # Parent No. 5855835
| GENERAL INFORMATION:
| APPLICANT: Smith, Rodger | APPLICANT: Smith, Rodger | APPLICANT: Chiswell, David | APPLICANT: Chiswell, David | APPLICANT: Chiswell, Bardel J. APPLICANT: Chiswell, Revin | APPLICANT: Titmas, Michael J. APPLICANT: Kenten, John H. | APPLICANT: Kenten, John H. | APPLICANT: Wartin, Mark T. | APPLICANT: Williams, Richard O. | APPLICANT: Williams, Richard O. | APPLICANT: Williams, Richard O. | TITLE OF INVENTION: The Isolation and Production of | TITLE OF INVENTION: Catalytic Antibodies using Phage Technology | NUMBER OF SEQUENCES: 71
| CORRESPONDENCE ADDRESS: ADDRESSE: STREET: 1530 East Jefferson St. | STREET: 1530 East Jefferson St. | STATE: MD | COUNTRY: USA | STATE: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-UUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.4%; Score 123.5; DB 2; Best Local Similarity 32.3%; Pred. No. 1.8e-06; Matches 30; Conservative 17; Mismatches 43;
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                                                                                                                                                                                                                                                                                                                                                        8648.49USF1
                     PALING MAIR: 03-00-00-1590
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-0CT-1995
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 05-00-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.491
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acids TYPE: amino acids STRANDEDNESS: single TOPOLOGY: linear
05-JUN-1996
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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32.6%; Pred. No. 1.9e-06;
tive 18; Mismatches 36; Indels 10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 118, Application US/09214095D; Patent No. 6280987; GENERAL INFORMATION:
APPLICANT: Landry, Donald; TITLE OF INVENTION:
TITLE REFERENCE: 51400-A-PCT-US; CURRENT FILIGHTER: 1999-07-19; NUMBER OF SEQ ID NOS: 121
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0; SEQ ID NO 118
LENGTH: 113
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Sequence 118, Application US/09940727B

Patent No. 6913917

GENERAL INFORMATION:

TITLE OF INVENITON: APPLICATION SHIT-COCAINE CATALYTIC ANTIBODY

TITLE REFERENCE: 0575/51400-B

CURRENT APPLICATION NUMBER: US/09/940,727B

CURRENT FILING DATE: 2002-09-04

PRIOR APPLICATION NUMBER: 09/214,095

PRIOR PILLING DATE: 1998-12-28

PRIOR APPLICATION NUMBER: PCT/US97/10965
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ATTORNEY/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
REPERSINGE/DOCKET NUMBER: 0900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
TELEPHONE: 301-284-816
INFORMATION FOR SEQ ID NO: 59: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 32.0.
The 31, Conservative
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.3%; Score 123; DB 2; Length 113; Best Local Similarity 32.6%; Pred. No. 1.9e-06; Matches 31; Conservative 18; Mismatches 36; Indels
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ZUP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/081,037

FILING DATE: 13-VUN-1997

CLASSIFICATION: 530

ATTONINY AGENT INFORMATION:

REGISTRATION NUMBER: 34,202

REGISTRATION NUMBER: 34,202

REFERENCE/DOCKET NUMBER: 34,202

RELEPPATION INFORMATION:

TELEPPATION 1NFORMATION:

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TELEPPATION 1NFORMATION:

TELEPPATION 1NFORMATION:

TELEPATION 1NFORMAT
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; Patent No. 6080588;
GENERAL INFORMATION:
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
PRIOR FILING DATE: 1997-06-25
PRIOR APPLICATION WUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
SEQ ID NO 118
LENGTH: 113
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SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
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STRANDEDNESS: single
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TOPOLOGY: linear
US-08-881-037-14
                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: mouse
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05x508 pongo pygma
065431 macaca mula
065930 homo sapien
09wur5 cavia porce
P01831 mus musculu
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1 QVSRGQKVTSLTACLVDQSL.......VLRDKLVKCEGVYYRYYFDY 111
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GenCore version 5.1.6
Copyright (c) 1993' - 2005 Compugen Ltd.
                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                        2166443 seqs, 705528306 residues
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THY1_MACMU
QS9GA0_HUMAN
QS9WURS_CAVPO
THY1_MOUSE
QS3YXZ_MOUSE
THY1_RAI
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092459 MOUSE

091467 MOUSE

091481 MOUSE

091481 MOUSE

092402 MOUSE

092402 MOUSE

091473 MOUSE

092407 MOUSE

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HVO5 MOUSE
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Q7TMK1 MOUSE
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Maximum Match 100%
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Q9GYZ2_MOUSB HV50_MOUSB Q924FA_MOUSB Q924FS_MOUSB HV49_MOUSB HV49_MOUSB Q924QI_MOUSB Q924QI_MOUSB Q924QI_MOUSB Q924QI_MOUSB Q924RO_MOUSB Q924RO_MOUSB Q924RO_MOUSB Q924RO_MOUSB Q924RO_MOUSB Q924RO_MOUSB Q924RO_MOUSB	ALIGNMENTS PRT; 161 AA. uence update)	Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CDW90) (CD90) antigen). Mame-THY1, Homo sapiens (Human). Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae, NCB1_TaxID=9606;	SOTIDE SEQUENCE.  INE=86016759, PubMed=2864690;  T., Spurr N., Obata F., Goyert S., Goodfellow P., Sil. human Thy-1 gene: structure and chromosomal location. Natl. Acad. Sci. U.S.A. 82:6657-6661(1985).	NUCLECTIDE SEQUENCE. MEDLINE=20403900; PubMed=10944468; DOI=10.1006/bbrc.2000.328 Ye Z., Connor J.R.; TONS Cloning by amplification of circularized first strand reveals non-IRE-regulated iron-responsive mRNAs."; Biochem. Blophys. Res. Commun. 275:223-227(2000).	LARGE SCALE MRNA]. rtium; to the EMBL/GenBank/DDBJ databases	NUCLECILES SEQUENCE (LARKOS SCALE MANA).  TISSUE=Brain, and Eye; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L.; Feingold B.A.; Grouse L.H., Derge J.G., A Altechul S.F., Zeeberg B., Buetow K.H.; Schaefer C.F., Bhat N.K., A Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko. L., Marutaina K., Farmer A.A.; Rubin G.M.; Hong L., B. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E B. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rahby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A Whiting M., Madan A., Young A.C., Sheychenko Y., Boulek and G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smail Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	00081 (Re (Re	membrane glycc (en). THY1; sapiens (Human) yota; Metazoa; 'lia; Eutheria; TaxID=9606;	NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. MEDLINE=86016759; PubMed=2864690; Seki I., Spurr N., Obata F., Goye "The human Thy-1 gene: structure Proc. Natl. Acad. Sci. U.S.A. 82:	SEQUENCE 403900; Proof J.R.; Ing by amin-IRE-regional Approximation of the proof of	SEQUENCE [LARGE gdala; cons consortium (MAR-2000) to the	skudukuch 11, skudukuch 18.L., Fre- 18.L., Zeebb F., Jordan M.J., Warun M.J., Warun M.C., Mush M.C., Mush M.C., Mush M.C., Mush M.C., Mush M.C., Mush M.C., Mush	A.C., Gr d Y.S.N.
1001 1001 1001 9000 9000 9000 9000	11 1 HUMAN THY1 HUMAN 204216; Q16 208-1987 28-FBB-2093 10-MAY-2005	Thy-1 membrane antigen). Name=THY1, Homo sapiens (H Eukaryota; Meta Mammalia; Euthe Homo.		MUCLEOTIDE MEDLINE=20 Ye Z., Con "CDNA Clon reveals no Biochem. B	TISSUE-Amygdala; TISSUE-Amygdala; The German CDNA Submitted (MAR-2	NUCLECTIDE NUCLECTIDE MEDLINE=22: Straugherg Straugherg Altachul S Hopking R.) Blodatchenko Stapleton I Brownstein Brownstein Brownstein Raha S.S., Richards S Villalon D Fahey J., Mhiting M.	driguez tterfiel hnerch A
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 1 THY1_HUMAN ID THY1_ AC P0421 DT 20-MA DT 28-FE DT 10-MA	H H H H H H H H H H H H H H H H H H H	MEDL NUCL Seki The	MED WED FE	TIS The The	ME STATE OF	San
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MACMU
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                                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                    use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 QVSRGQKVTSLTACLVDQSLRIDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTY 74
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                                                 MUCLEOTIDE SEQUENCE OF 1-55.

MEDLINE=93340114; PubMed=7683034; DOI=10.1084/jem.177.5.1331;

Craig W., Kay R., Cutler R.L., Lansdorp P.M.;

"Expression of Thy-1 on human hematopoietic progenitor cells.";

J. Exp. Med. 177:1331-1342(1993).

-! FUNCTION: May play a role in cell-cell or cell-ligand interactions during synaptogenesis and other events in the brain.

-! SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

-! SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
Generation and initial analysis of more than 15,000 full-length human
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Removed in mature form.
Ig-like V-type.
GP1-anchor amidated cysteine.
N-linked (GlcNAc. .).
By similarity.
If -> AP (in Ref. 5).
If -> AP (in Ref. 1).
N-> H (in Ref. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prem; Product; 1. SMART; SM00409; IG; 1. SMART; SM00409; IG; 1. PROSITE; PS50835; IG_LIKE; 1. Glycoprotein; GFI-anchor; Immunoglobulin domain; Lipoprotein; Membrane; Signal; T-cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 424; DB 1; Length 16
Pred. No. 8.8e-37;
3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane; TAS
             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                EMBL; M11749; AAA61180.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                           Ensembl, ENSG0000154096; Homo sapiens.
HGNC; HGNC:11801; THY1.
H-InvDB; HIX0010195; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005887; C:integral to plasma me GO; GO:0005886; C:plasma membrane; NAS; InterPro; IPR003599; Ig. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                           EMBL; AF261093; AAG13904.1; -; mRNA.—
EMBL; AL161958; CAB82106.1; -; mRNA.
EMBL; BC005175; AAH05175.1; -; mRNA.
EMBL; BC06559; AAH6559.1; -; mRNA.
EMBL; SS9749; AAB26353.2; -; mRNA.
PIR; A02106; TDHU.
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Best Local Similarity 73.9%;
Matches 88; Conservative
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RESULT 2 QSR508 PONPY ID QSR508_PONPY PRELIMINARY;

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Margulies B.J., Clements J.E.;
Margulies B.J., Clements J.E.;
Whegus macaque CD90.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May play a role in cell-cell or cell-ligand interactions during synaptogenesis and other events in the brain.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRKKHVLFGTID-PADSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                  Blocker H. Boecher M., Brandt P., Mewes H.W., Weil B., Amid Obanger A., Fobo G., Han M., Wiemann S.;
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CR861077, CAP93188.1; -; mRNA.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
FAMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
Hypochetical protein; Immunoglobulin domain.
SEQUENCE 161 AA; 17963 MW; 286791DDBCE0401B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CDw90)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 161;
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Created)
Last sequence update)
Last annotation update)
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                                                                Hypothetical protein DKFzp459C1015.
Name=DKFZp459C1015;
(TrEMBLrel. 29, (TrEMBLrel. 29,
                                                                                                                                                                                                                                                                                                 The German cDNA Consortium;
                                                                                                                  Pongo pygmaeus (Orangutan)
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01-FEB-2005 (TrEMBLrel
01-FEB-2005 (TrEMBLrel
01-FEB-2005 (TrEMBLrel
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                                                                                                                                                                                                           NCBI_TaxID=9600;
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60 TS------YNQNF--KDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGV 103
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Name-Thyl; Synonyms=Thy-1;

Num musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;

Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
MEDITNE-85115360; Pubbed=2857501;
Seki T., Chang H.-C., Moriuchi T., Denome R., Ploegh H., Silver J.;
"A hydrophobic transmembrane segment at the carboxyl terminus of thy-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CDw90) (CD90
                                                                                                              Cavia porcellus (Guinea pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                          TISSUB-splen;
Schaefer H., Burger R., Otto A., Bartels T.;
Schaefer H., Burger R., Otto A., Bartels T.;
Characterization and cloning of guinea pig Thy-1.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
R EMBL; AJ23889; CAB44008.1; -; mRNA.
R InterPro; IPR003599; Ig.
R InterPro; IPR00710; Ig-1ike.
R Ffam; PR0047; ig. 1.
R Ffam; PR0047; ig. 1.
R SWART; SM00409; IG. 1.
R PROSITE; PS50835; IG LIKE; 1.
R RNART; SM00409; IG. 1.
R PROSITE; PS50835; IG LIKE; 1.
R TIMULOGIODULIN domain; Signal.
FIGNAL 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.9%; Score 332; DB 2; Length 161; 60.5%; Pred. No. 5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN 20 161 Thy-1 protein. SEQUENCE 161 AA; 17995 MW; 241461D901F80B1B CRC64;
                                                        Last sequence update)
Last annotation update)
  161 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/c;
MEDLINE=8665576; PubMed=2866091;
Giguere V., ISODE K.-I., Grosveld F.;
"Structure of the murine Thy-1 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPE)
PRT;
                                      Created)
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21-JUL-1986 (Rel. 01, Last seq
10-MAY-2005 (Rel. 47, Last anno
                                01-NOV-1999 (TrEMBLrel. 12, 0
01-NOV-1999 (TrEMBLrel. 12, 1
01-OCT-2003 (TrEMBLrel. 25, 1
Thy-1 protein precursor.
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Q9WUR5 CAVPO PRELIMINARY;
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                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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ID THY1 MOUSE
AC P01831;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 IS-----YNQ-----NPKDEGTYTCALHHSGHSPPISSGNVTVLRDKLVKCEGV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 RSRINFTSKYNMKVLYLSAFTXKDEGTYTCKLHHSGHSPPISSQNVTVLRDKLVKCEGI 133
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTID-PADSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S., Ohara O., Nagase T., Kikuno P.R.;
"None Title.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AB209209; BAD92446.1; -; mRNA.
                                                                                                                                                                                                      Ig-like V-type.

GPI-anchor amidated cysteine.
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 RSRINFISKYNMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 TS-----YNONF-----KDEGTYTCALHHSGHSPPISSONVTVLR 94
              InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
Pfam; PR00047; ig. 1.
SMART; SM00409; IG; 1.
PR0STTR; PSS51835; IG, LIKE; 1.
MG1YCOPCOFELSI, GPLARCHOF; Immunoglobulin domain; Lipoprotein;
Membrane; Signal; T_cell.
                                                                                                                                                                                                                                                                                                                                                                                                    68.9%; Score 417; DB 1; Length 161;
llarity 72.3%; Pred. No. 4.9e-36;
Conservative 4; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.3%; Score 377; DB 2; Length 145; ilarity 72.7%; Pred. No. 7.5e-32; Conservative 2; Mismatches 12; Indels 1
                                                                                                                                                                      Thy-1 membrane glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                  326B135498BA401B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 AA; 15904 MW; 9DA4BC208DCD5766 CRC64;
                                                                                                                                                                                          Removed in mature form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Thy-1 cell surface antigen variant (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 AA
                                                                                                                                                                                                                                                                                                                          By similarity.
By similarity.
  EMBL; U93310; AAC05640.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                  18011 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q59GAO_HUMAN PRELIMINARY;
Q59GAO;
                                                                                                                                                                                        161
126
130
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                                                                                                                                                                                                                                                                                                                                                                    161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
ses 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Q9WURS_CAVPO
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NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPE)

Best Loca Matches

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Gaps

16;

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STRAIN=FVB;
                  DOMAIN
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ID THY1 RAT
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                                                                                                                                               DISULFID
                                                                                                                                                                                SEQUENCE
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                                                                                                           CARBOHYD
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WEDLINE-2188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RICHARDER R.D., Felngold E.A., Grouse L.H., Derge J.G.,

RICHARDER R.D., Colling F.S., Margner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bronstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabb R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabb R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabb R.A.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gubs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gubs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gubs R.A.,

Raha S., Worley K.C., Hale S., Garcia A.W., Gubs R.A.,

Raha S., Worley K.C., Hale S., Garcia A.W., Gubs R.A.,

Raha S., Worley K.C., Hale S., Garcia A.W., Gubs R.A.,

Raha S., Worley K.C., Hale S., Garcia A.W., Gubs R.A.,

Raha S., Worley K.C., Hale S., Garcia A.W., Gubs R.A.,

Raha S., Worley K.C., Hale S., Garcia A.W., Gubs R.A.,

Raha S., Worley K.C., Marchan J., Notrigues S., Sanchez A.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

Radriguez A.C., Grimmal J.M., Rodrigues G. G.,

Radriguez A., Schein J.B., Worley R.W.,

Radrig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-85216583; PubMed-2582427;
Chang H.-C., Seki T., Moriuchi T., Silver J.;
"Isolation and characterization of mouse Thy-1 genomic clones.";
Proc. Natl. Acad. Sci. U.S.A. 82:3819-3823(1985).
                                                                                                                      Ingraham H.A., Lawless G.M., Evans G.A.;
"The mouse Thy-1.2 glycoprotein gene: complete sequence and identification of an unusual promoter.";
J. Immunol. 136:1482-1489 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR07110, Ig-like.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Glycoprotein; GPI-anchor;
Immunoglobulin domain; Lipoprotein; Membrane; Polymorphism;
Pyrrolidone carboylic acid; Signal; T-cell.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thy-1 membrane glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A94278; TDMS.
Ensembl; ENSMUSGO0000022011; Mus musculus.
MGI; MGI:98747; Thyl.
GO; GO:0009897; C:external side of plasma membrane; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X03151; CAA26930.1; -; Genomic_DNA.

EMBL; X02771; CAA26548.1; -; Genomic_DNA.

EMBL; X02772; CAA26549.1; ALT SEQ; Genomic_DNA.

EMBL; X02773; CAA26550.1; ALT_SEQ; Genomic_DNA.

EMBL; M10246; AAA40440.1; -; Genomic_DNA.

EMBL; M1279; AAA40441.1; -; Genomic_DNA.

EMBL; M1279; AAA40443.1; -; Genomic_DNA.
                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC054436; AAH54436.1; -; mRNA.
                                                                                                           MEDLINE=86113437; PubMed=2868059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           removed.
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EMBL;
EMBL;
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59 Y----TSYNQ------NF--KDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 YRSRVTLSNQPYIKVLTLANFTTKDEGDYFCELRVSGANPMSSNKSISVYRDKLVKCGGI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 Y----TSYNQ------NF--KDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 YRSRVILSNQPYIKVLTLANFITKDEGDYFCELQVSGANPMSSNKSISVYRDKLVKCGGI 134
                                                                                                                                                                                                                                                                                                                                                                                                                             74
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                                                                                                                                                                                                                                                                                                                                                                                 1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMH-FSLTRETKKHVLFGTID-PADS
                                                                                                                                                                                                                                                                                                                                                                                                            QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMH-FSLTRRTKKHVLFGTID-PADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delaitre E., Jean L., Tron F., Boyer O.; "A single amino acid substitution confers CD90.1 (Thy1.1) allotype
                                                                                                                                                                                                                                                                                                                                  23; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.2%; Score 291.5; DB 2; Length 162; 55.8%; Pred. No. 9.9e-23; indels 17:ive 13; Mismatches 23; Indels 17
                                                                                                                                                                                                                                                                                     DB 1; Length 162;
                                                                  GPI-anchor amidated cysteine.
N-linked (GlCNAc. .).
N-linked (GlCNAc. .).
N-linked (GlCNAc. .).
                      Ig-like V-type.
Pyrrolidone carboxylic acid
                                                                                                                                                                                                             108 Q -> R (in allele Thy-1.1).
18080 MW; 3978F7D3A9F2C77B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specificity.";
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, A444563; ARR17087.1; -; mRNA.
Ensembl; ENSMUSGO000032011; Mus musculus.
MGI; MGI:98747; Thyl.
GO; GO:0009897; C:external side of plasma membrane; IDA.
InterPro; IPR007110; Ig-1ike.
InterPro; IRR003596; Ig_v.
SMART; SM00406; IGv.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain.
SEQUENCE 162 AN; 18108 MW; 6978F4D3A9F2C530 CRC64;
  Removed in mature form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                   48.2%; Score 291.5; DB 1
55.8%; Pred. No. 9.9e-23;
iive 13; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67; Conservative
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                                                                                                                                                                                                                                                                                                                                       67, Conservative
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162
127
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94
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105
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                                                                                                                                                                                                                                      162 AA;
                                                                                                                                                                                                                                                                                                           Local Similarity
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Best Local Similarity
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-i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-i- TISSUB SPECIPICITY: Abundant in lymphoid tissues by a GPI-anchor.
-i- PTM: Glycosylation is tissue specific. Sialylation of N-glycans at Asn-93 in brain and at Asn-42, Asn-93 and Asn-117 in thymus.
-i- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE OF CARBOHYDRATES.
STRUCTURE OF CARBOHYDRATES.
MEDLINE-87275814; PubMed=2886334;
PARELINE-87275814; PubMed=2886334;
Parekh R.B., Tse A.G.D., Dwek R.A., Williams A.F., Rademacher T.W.;
"Tissue-specific N-glycosylation, site-specific oligosaccharide
patterns and lentil lectin recognition of rat Thy-1.";
EMBO J. 6:1233-1244(1987).
                21-JUL-1986 (Rel. 01, Created)
13-MUS-1987 (Rel. 05, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CDw90) (CD90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE OF 20-161.
MEDLINE-85051865; PubMed-6149956; DOI=10.1016/0014-5793(84)81250-8;
Moriuchi I., Silver J.;
"Rat Thy-1 antigen has a hydrophobic segment at the carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN SEQUENCE OF 20-130.
MEDLINE=82068190; PubMed=6118137;
Campbell D.G., Gagnon J., Reid K.B.M., Williams A.F.;
Rat brain Thy-1 glycoprotein. The amino acid sequence, disulphide bonds and an unusual hydrophobic region.";
Biochem. J. 195:15-30(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Moriuchi T., Chang H.-C., Denome R., Silver J.; "Thy-1 cDNA sequence suggests a novel regulatory mechanism."; Nature 301:80-82(1983).
                                                                                                                                                                                                                                                                     MEDLINE-86005549; PubMed=2864289; Seki T., Chang H.-C., Moriuchi T., Denome R., Silver J.; "Thy-1: a hydrophobic transmembrane segment at the carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLECTIDE SEQUENCE OF 20-161.
MEDLINE-85111162; PubMed=2857477;
Seki T., Moriuchi T., Chang H.-C., Denome R., Silver Structural organization of the rat thy-1 gene.";
Nature 313:485-487(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X03152; CAA26931.1; -; Genomic_DNA.
EMBL; X03150; CAA26929.1; -; mRNA.
EMBL; X02002; CAA26033.1; -; Genomic_DNA.
EMBL; M18002; AAA42243.1; -; mRNA.
EMBL; M10666; AAA42242.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=83115223; PubMed=6130472;
                                                                                                                                                                                                                                                                                                                                                        Fed. Proc. 44:2865-2869(1985).
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'RBS Lett. 178:105-108(1984)
                                                                                                                 Name=Thy1; Synonyms=Thy-1;
                                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                     terminus.";
                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE
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15 QMSRGQRVISLTACLVNQNLRLDCRHENNTNLPIQHEFSLTREKKKGHVLSGTLGVPEHTY 74
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                                                                                                                                                                                                                                                                                                                                                                                                                   complex); in thymus.
N-linked (GlcNAc. . .) (high mannose); in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTID-PADSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=14711516; DOI=10.1016/j.pep.2003.10.011; MehbMed=14711516; DOI=10.1016/j.pep.2003.10.011; MehbMed=14711516; DOI=10.1016/j.pep.2003.10.011; Mehbdiratta P., Warthall A.G., Logan T.M.; Pulido S., Parthagarathy G., Emmett M.R., Warghall A.G., Logan T.M.; ization of avian Thy-1 from Lec1 mammalian and Tn5 insect cells."; Protein Expr. Purif. 33.274-287(2004). Protein Expr. Purif. 33.274-287(2004). EmBl. AV230132; AAP31241.1; -7 mRNA. Ensembl; ENSGALGO000006751, Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .) (high mannose or
                                                                                                                                                                                                                                                                                                                                                                                          N-linked (GlcNAc. . .) (high mannose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 280; DB 1; Length 161;
; Pred. No. 1.6e-21;
16; Mismatches 27; Indels 1
                                                                                                                                                                                                                                                                                                                                          Pyrrolidone carboxylic acid. GPI-anchor amidated cysteine
                                                                                                                                                                                                                       Pyrrolidone carboxylic acid; Sialic acid; Signal; T-cell.
                                                                                                                                                                                                                                                                  Thy-1 membrane glycoprotein.
Removed in mature form.
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104
71
18172 MW, 3285748F3C2C5AB2 CRC64;
Ensembl; ENSRNOG0000006604; Rattus norvegicus.
RGD; 3860; Thyl.
GO; GO:0009986; C:cell surface; TAS.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
SMART; SM00409; IG, 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50836; IG LIKE; 1.
Inter protein sequencing; Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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N-linked
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N-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain.
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InterPro; IPR007110; Ig-11ke.
Pfam; PF00047; ig; 1.
SMRAT; SW00409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTT252_CHICK PRELIMINARY;
Q7T252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60; Conservative
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38
71
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MOD_RES
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Matches
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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DISULFID
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       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                 1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGT1DPADS-Y 59
                                                                                                                                                                          15 QAAHCQMIRDLSACLLGQSLRVDCRYENKTSDPLTYEFSLTKDNRKHIIQSTISVSENVY 74
                                                                                                                                                                                                                                                                             60 TS------YNONF--KDEGTYTCALHHSGHSPPISSONVTVLRDKLVKCEG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycoprotein.";
Brain Res. Mol. Brain Res. 14:250-260(1992).
-!-FUNCTION: May play a role in cell-cell or cell-ligand interactions during synaptogeneeis and other events in the brain.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: Forebrain, cerebellum and tectum.
-!- TISSUE SPECIFICITY: Forebrain, cerebellum and tectum.
-!- DEVELOPMENTAL STAGE: It is detected at embryonic day 4 (E4) in forebrain and tectum. There is an increase in levels between E16 and the first few days post-hatch. During E19 to hatch a rapid reduction in the levels is seen with a general increase in expression in adulthood.
-!- PTM: The N-terminus is blocked.
-!- FTM: Contains 1 Ig-like V-type (immunoglobulin-like)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin domain; Lipoprotein; Membrane;
Pyrrolidone carboxylic acid; Signal; T-cell.
SIGNAL 1 19 By similarity.
20 129 Thy-1 membrane glycoprotein.
PROPEP 130 160 Removed in mature form (By similarity).
MOD_RES 20 20 Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 43-55; 59-79 AND 81-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=White leghorn; TISSUG-Brain; MEDLINE-3066794; PubMed=1359371; DOI=10.1016/0169-328X(92)90180-J; MEDLINE-396601794; PubMed=1359371; DOI=10.1016/0169-328X(92)90180-J; DOWSLING B.J., Gooley A.A., Gunning P., Cunningham A., Jeffrey P.L.; Molecular cloning and primary structure of the avian Thy-1
                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
GPI-anchor amidated cysteine (By
similarity).
                                             Query Match 31.2%; Score 189; DB 2; Length 160; Best Local Similarity 35.6%; Pred. No. 7.2e-12; Matches 42; Conservative 22; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Thy-1 membrane glycoprotein precursor (Thy-1 antigen).
18061 MW; 6DC39D8519540CE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003599; Ig.
SMART; SM00409; IG; 1.
Direct protein sequencing; Glycoprotein; GPI-anchor;
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Ensembl; ENSGALG0000006751; Gallus gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 547368; AAA11889.1; -; mRNA.
EMBL; L14924; AAC42216.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
  160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus.
NCBI_TaxID=9031;
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  SEQUENCE
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Pubmed=7525684;
Pokuluri P.R., Bouthillier F., Li Y., Kuderova A., Lee J., Cygler M.;
Pokuluri P.R., Bouthillier F., Li Y., Kuderova A., Lee J., Cygler M.;
Preparation, characrerization and crystallization of an antibody Fab fragment that recognizes RNA. Crystal structures of native Fab and three Fab-monouclectide complexes.";
J. Mol. Biol. 243:283-297(1994).
BMBL, AB069916; BAB63932.1; -; mRNA.
PIR; PH1160; PH1161.
PIR; PH1161; PH1161.
PIR; PH1161; PH1162.
PIR; PH1162; PH1162.
PIR; S53751; S53751.
HSSP, P01751; JA6W.
Ensembl; ENSMUSG00000061773; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                   15 QAAHCQMIRDLSACLLGQSLRVDCRYENKTSNPLTYBFSLTRQ-QKHIIQSTISVSENVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 RNRANVTWHKNLVCLYLHSFTTSDEGVYMCELKATNDYTGNQIKNITVIKDKLEKC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                         Gaps
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                              (Potential).
(Potential).
(Potential).
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     N-linked (GlcNAc. ..) (Potential)
N-linked (GlcNAc. ..) (Potential)
N-linked (GlcNAc. ..) (Potential)
By similarity.
By similarity.
R > F (In Ref. 1; AA sequence).
H -> I (In Ref. 1; AA sequence).
W; E378D241CC2D4739 CRC64;
                                                                                                                                                                                                                                                            DB 1; Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.8%; Score 132; DB 2; Length 143; 28.2%; Pred. No. 7e-06;
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                                                                                                                                                                                                                                                                                                         35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 143 143 15704 MW; 43CD8C72D52134F6 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                      29.2%; Score 176.5; DB 1 36.2%; Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 AA
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                                                                                                                                                                                                                                                                                                       22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V303-D-J-C mu protein (Fragment)
Name=V303-D-J-C mu;
42
78
118
138
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103
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R
18165 MW;
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InterPro; IPR003596; Ig v.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q924P9_MOUSE PRELIMINARY;
Q924P9;
                                                                                                                                                                                                                                                                                Local Similarity 36.2 tes 42; Conservative
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PH1147;
PH1149;
                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q924R8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR;
PIR;
PIR;
PIR;
                                                                                                                                                                                                                                                                                                                           Matches
with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 STAYMQLSSLISEDSAVYYCASHYYGSSSDYWGQGTTLTVSSESQSFPNVFPLVSCE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/c;
MEDIINE=20448942; PubMed=10992488;
DOI=10.1128/1AI.68.10.5803-5808.2000;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
  -------DEGTYTCALHHSGHSPPISSONVTVLRDK-------LVKCB 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;

Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalla, Butheria, Buarchontoglires, Glires; Rodentia, Sciurognathi;
Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 29, Last annotation update)
v4186.2-D-3-C mu protein (V304-D-3-C mu protein) (Fragment).
Name=VH186.2-D-3-C mu; Synonyms=V304-D-3-C mu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 33.7%; Pred. No. 1.1e-up;
Best Local Similarity 33.7%; Pred. No. 1.1e-up;
Matches 31; Conservative 15; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 AA; 15775 MW; 91BC6012B44EFEBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 SGHSPPISSQNVTVLRDKLVKCEGVYYRYYFD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :|| :|| STAYMQLSS--LTSEDSAVYYCAPTVDDWYFD 106
                                                                                                                                            143 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P01751; 1A6W.
SMR; Q91V67; 1-129.
Ensembl; ENSMUSG0000021155; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kozono Y., Kozono H., Azuma
Submitted (AUG-2001) to the
EMBL, AB069912; BAB63928.1;
EMBL, AB069914; BAB63930.1;
PIR; S26744; S26744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JL81 MOUSE
ID Q9JL81 MOUSE PRELIMINARY;
AC Q9JL81;
                                                                                                                                    Q91V67 MOUSE PRELIMINARY;
Q91V67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6;
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  89
                                                                                                 RESULT 12
091067 MOU
10 09106
AC 09106
DT 01-DB
DT 01-PB

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.; "Allogeneic manipulation of the GAT idiotypic cascade. Immunization C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-specific V genes as the original antigen."; J. Immunol. 141:779-784 (1988).

EMBL; AB067781; BAB63266.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                            Length 114;
                                                                                                                                                                                                                                                                                                                                    20.8%; Score 126; DB 2; Length 11 32.0%; Pred. No. 2.3e-05; tive 11; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 SGHSPPISSQNVTVLRDKLVKCEGVYY-------RYYFDY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 ----DKSSSTAYMQLSSPTSEDSAVYYCARSNYYGSSLYYFDY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kozono Y., Kozono H., Azuma T., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                     114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 AA
                                                                                ASST, 50.716.

BRNEWD1; ENSWISSONONOO1155; Mus musculus.

INTERPRO; IPROO7110; Ig-1ike.

INTERPRO; IPRO03596; Ig v.

SMART; SM00406; IGv; 1.

PROSITE; PSS0835; IG_LIKE; 1.
            Infect. Immun. 68:5803-5808(2000).
EMBL; AF206025; AAF69323.1; -; mRNA.
HSSP; P01751; INQB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VH186.2-D-J-C mu protein (Fragment)
Name=VH186.2-D-J-C mu;
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 32.0%
hes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q924R8_MOUSE PRELIMINARY;
cardiac myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PH1114.
PH1118.
PH1119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; F28833; F28833.
PIR; PH1105; PH1105.
PIR; PH1108; PH1108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PH1126.
PH1128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
PubMed=3135311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6
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MEDINE=23380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.D., Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,
Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A. McEwan P.J., McKerran K.J., Malek J.A., Gunaratne P.H.,
Bosak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzuy D.W., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski W.I., Skalska U., Smailus D.E.,
M. Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 SLRLDCRHENTSSSNYMMHFSLTRETKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentía; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 19.6%; Score 118.5; DB 2; Length Best Local Similarity 32.3%; Pred. No. 0.00019; Matches 31; Conservative 13; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL, 8C094936; AAH94936.1; -; mRNA. InterPro; IPR003599; Ig. InterPro; IPR007100; IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                      146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/GNCr; TISSUE=Hematopoietic Stem Cell;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 STAYMOLSS--LTSEDSAVYYCARSYYGSSLYYFDY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 SGHSPPISSQNVTVLRDKLVKCEGVYY---RYYFDY 111
PIR; PH1150; PH1150.

PIR; PH1151; PH1151.

PIR; PH1152; PH1152.

PIR; PH1153; PH1153.

HSSP; P01751; 1A6W.

SMR; Q924R8; 1-137.

Ensembl; ENSWIGGO000021155; Mus musculus.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

SMART; SM00406; IGV; 1.

PR051TE; PS50815; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q504M7_MOUSE PRELIMINARY;
Q504M7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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NON TER
SEQUENCE
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0504M7 MOUT
10 0504M7 MOUT
13 -SE
DT 13 -SE
DT 13 -SE
DT 13 -SE
DE HYPOT
050 MAINT
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Search completed: December 6, 2005, 10:41:50 Job time : 115.094 Becs

Thu Dec

# 5.1.6 Compugen Ltd. GenCore version Copyright (c) 1993 - 2005

- protein search, using sw model OM protein 6, 2005, 10:32:12; Search time 103.652 Seconds (without alignments) 470.529 Million cell updates/sec December Run on:

Title: Perfect score:

US-10-611-655-4 605 1 QVSRGQKVTSLTACLVDQSL......VLRDKLVKCEGVYYRYYFDY 111 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2443163 seqs, 439378781 residues Searched:

2443163

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_21:* Database

geneseqp2003bs:*geneseqp2004s:* geneseqp2002s:* geneseqp2003as:* geneseqp20008:* geneseqp20018:* geneseqp1980s:* geneseqp1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:*

		Description	Adw10186 Thy-1 bas	Adp65208 Human Thy	Abo84755 Human can	Adz13572 Human can	Adz13574 Human can	Adz13570 Human can	Aab43939 Human can	Aag73850 Human col	Abb90744 Human Tum	Human	Human	Adw10183 Human Thy	_	_	_	Aay31787 Human Thy	Adk98542 Human imm	Abb90786 Mouse Tum	Abu54493 Mouse tum	_	Adz13567 Murine ca	Abg19538 Novel hum	Aaw53480 Rat THY-1	Aay31788 Rat Thy-1
SUMMARIES		ΕĐ	ADW10186	ADP65208	AB084755	ADZ13572	ADZ13574	ADZ13570	AAB43939	AAG73850	ABB90744	ABU54451	AAY31789	ADW10183	ADW10192	ADW10190	ADW10188	AAY31787	ADK98542	ABB90786	ABU54493	AB084754	ADZ13567	ABG19538	AAW53480	AAY31788
		80	6	7	œ	6	σ	σ	m	4	ß	9	~	σ	σ	σ	σ	~	8	Ŋ	9	æ	σ	4	7	7
		Match Length	111	191	161	191	191	161	165	165	191	191	368	162	176	334	334	119	150	162	162	162	162	171	161	368
de	Query	Match	100.0	70.1	70.1	70.1	70.1	70.1	70.1	70.1	69.8	69.8	69.3	66.5	65.8	65.8	65.8	65.3	62.3	48.2	48.2	48.2	48.2	48.1	46.3	45.8
		Score	605	424	424	424	424	424	424	424	422	422	419	402.5	398	398	398	395	377	291.5	291.5	291.5	291.5	291	280	277
	Result	No.	1	7	٣	4	'n	9	7	۵	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Addil2417 Mouse Thy Adg3435 Mouse Thy Adg31786 Rat Thy-1 Adg0166 Human sec Ady27074 Monoclona Adw10184 Human ant Adg1953 Novel hum Adg79380 Thyrotrop Adg79380 Thyrotrop Adg79380 Thyrotrop Adg79380 Thyrotrop Adg79380 Thyrotrop Adg7938 Biosynthe Add3995 Antibody Adg80148 Biosynthe Add3995 Antibody Adg80148 Biosynthe Add5855 GAUG	
ADF12417 ADG39435 AAX31786 AAX20166 AAX27074 ADN10184 ABG19536 ADP79380 ADP79380 ADP79380 ADP79380 ADP79380 ADP73384 AAB61953 ADP39962 ADF339962 ADF33983 ADF34450 ADF34450 ADF34450 ADF374450	AAW00831 AAW19017
C 8 0 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1010
114 1119 1105 124 124 124 1124 1117 117 117 117 117 117	117
4444 4444 80000000000000000000000000000	20.7
264.5 264.5 242.56 242.56 198.5 143.5 143.5 128.5 128.5 128.5 128.5 128.5 128.5 128.5	125
22222222222222222222222222222222222222	44.45

### ALIGNMENTS

ADW10186 standard; protein; 111 AA. RESULT 1 ADW10186 

ADW10186;

(first entry) 24-MAR-2005 Thy-1 based ThyOx non-immunoglobulin binding polypeptide, SEQ ID 4.

non-immunoglobulin binding polypeptide; selective binding; ThyOx.

Synthetic.

US2004266993-A1.

30-DEC-2004.

30-JUN-2003; 2003US-00611655.

30-JUN-2003; 2003US-00611655.

(EVAN/) EVANS G A.

Evans GA;

WPI; 2005-047648/05.

New chimeric non-immunoglobulin binding polypeptide comprises immunoglobulin-like domain containing scaffold and exhibits selective binding activity, for producing non-immunoglobulin binding polypeptides with selective binding activity.

Disclosure; SEQ ID NO 4; 45pp; English.

The invention relates to a novel chimeric non-immunoglobulin binding polypeptide. The polypeptide comprises an immunoglobulin-like domain containing a ccaffold with two or more solvent exposed loops containing a different complementarity-determining region (CDR) from a parent antibody inserted into each of the loops and exhibiting selective binding activity toward a ligand bound by the parent antibody. The invention further comprises: a chimeric ThyOx binding polypeptide, comprising one or more altered immunoglobulin-like domain loop regions of a ThyOx family polypeptide or at least one immunoglobulin-like domain containing scaffold derived from a ThyOx family polypeptide, and a heterologous binding polypeptide exhibiting selective binding activity toward a non-ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx

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                                                                                                                                                                                                                                                              Q'SRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHPSLTRETKKHVLFGTIDPADSYT
binding polypeptide above. The chimeric non-immunoglobulin binding polypeptide is useful for producing non-immunoglobulin binding polypeptides having selective binding activity toward a predetermined molecule. This sequence represents a Thyox non-immunoglobulin binding
                                                                                                                                                                                                                                      QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTIDPADSYT
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                 61 SYNQNFKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGVYYRYFDY 111
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                                                                                                                                                             Length 111;
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                                                                                                                                                         100.0%; Score 605; DB 9;
100.0%; Pred. No. 1.8e-57;
ive 0; Mismatches 0;
                                                                            polypeptide of the invention.
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                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                     Sequence 111 AA;
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Ź ADP65208 standard; protein; 161 (first entry) 12-AUG-2004 ADP65208; 

Human Thy-1 cell surface antigen, Thy-1 T-cell antigen.

RESULT 3

AB08475

autoimmune disease; arthritide; gene expression analysis; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antigout; antiinflammatory; dermatological; immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgis; osteoarthritis; gout; juvenile rheumatoid arthritis; immune; human

Homo sapiens,

WO2003072827-A1.

04-SEP-2003

31-OCT-2002; 2002WO-US035433

31-OCT-2001; 2001US-0336220P

(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

Thorton SL; Hirsch R,

WPI; 2003-712740/67. GENBANK; NP_006279.

Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and

Disclosure; Page; 56pp; English.

The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing sene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature of the mRNA, and using that of a rathritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis; in a mammal other than a mouse; diagnosis of rheumatoid arthritis in a mammal array or gene chip, specific for rheumatoid arthritis; diagnosis or

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analyses of autoimmune disease or rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collageninduced arthritis; and reducing the symptoms associated with collagenatiduced arthritis. The compositions of the invention have the following activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic, antigout, antiinflammatory, dermatcholgical, and immunomodulatory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease or arthritides, such as rheumatoid arthritis, lupus, ankyloaing spondylitis, fibrositis, in fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, und an immune disease caused by an infectious agent. This sequence represents a protein sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 RSRINFISKYNMKVLYLSAPISKDEGTYTCALHHSGHSPPISSONVIVLRDKLVKCEGI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 TS-----YNQNF-----KDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHPSLTRETKKHVLFGTID-PADSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 1.2e-37;
3; Mismatches 12
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Human, cancer-associated protein; CAP; cancer; cytostatic. Human cancer-associated protein (CAP) HP07-003. Ż ABO84755 standard; protein; 161 (SAGR-) SAGRES DISCOVERY INC. 17-DEC-2002; 2002US-00322281 15-DEC-2003; 2003WO-US040081 18-NOV-2004 (first entry) WO2004058146-A2 Homo sapiens. 15-JUL-2004. AB084755; 

Novel human cancer associated protein encoded within open reading f of cancer associated gene, useful as targets for diagnosing cancer. Claim 18; SEQ ID NO 20; 182pp; English. N-PSDB; ABD33081

Malandro

Morris DW,

WPI; 2004-499109/47.

The invention relates to cancer-associated proteins (CAP) and the cancer-associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer drug candidate and monitoring the effect of the anticancer drug candidate and monitoring the effect of the anticancer on expression of the CA gene. The CAP proteins are useful for detecting

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cancer associated with expression of a CAP protein in a test cell sample activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a human CAP of the invention. Note: The specification, but was obtained in electronic form part of the printed at ftp.wipo.int/pub/published_pct_sequences
    8888888888888
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Sequence 161 AA;

'n Gaps 16; Length 161; 12; Indels Score 424; DB 8; Pred. No. 1.2e-37; 3; Mismatches 12 Query Match
Best Local Similarity 73.9%;
Matches 88; Conservative

15 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTY 74 60 TS-----YNQNF-----KDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGV 103 1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTID-PADSY 셤 셤 ઠે ò

ADZ13572 RESULT

ADZ13572 standard; protein; 161 AA.

AD213572;

(first entry) 16-JUN-2005

Human cancer-associated protein #329.

Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm; cytostatic 

Homo sapiens.

WO2005031001-A2 07-APR-2005 23-SEP-2004; 2004WO-US031617.

23-SEP-2003; 2003US-00669920

(CHIR ) CHIRON CORP

Morris DW, Malandro MS;

WPI; 2005-273395/28. N-PSDB; ADZ13571 Nucleic acid array useful for detecting cancer associated nucleic acid, comprises two or more nucleic acid probes.

Disclosure, SEQ ID NO 1092; 198pp; English.

The invention relates to a nucleic acid array for detecting a cancer associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA nucleic acids are useful for detecting CA nucleic acids are acid and CA nucleic acids are acid and CA nucleic acids are acid and CA nucl

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associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more that binds polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA
                                                      the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual. The invention is a therspectic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA gene in a cell. This sequence represents a human cancer-associated protein of the
                                                                                                                                                                                                                                                                                                                     23
absence of cancer cells in an individual which involves contacting cells from the individual with the antibody and detecting a complex of a CA protein from the cancer cells and the antibody, where the detection of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
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                                                                                                                                                                                                                                        Score 424; DB 9; Length 161;
Pred. No. 1.2e-37;
3; Mismatches 12; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer-associated protein #330.
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                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                         Sequence 161 AA;
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                                                                                                                                                                    invention.
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nucleic acid in a cell. The CA nucleic acids are useful for detecting CA absence of cancer cells in an individual which involves contacting cells from the individual which involves contacting cells from the individual with the antibody and detecting a complex of a CA protein from the cancer cells and the antibody, where the detection of the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA gene in a cell. This sequence represents a human cancer-associated protein of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
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                                                                                                                                                                                                                                         73.9%; Score 424; DB 9; 73.9%; Pred. No. 1.2e-37;
                                                                                                                                                                                                                                                                        3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADZ13570 standard; protein; 161 AA
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associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more tables to a polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a

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method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA nucleic acid in a cell. The CA nucleic acids are useful for detecting CA nucleic acids. The antibody is useful for detecting the presence of cancer cells in an individual which involves contacting cells from the individual which involves contacting cells from the individual which the antibody and detecting a complex of a CA protein from the cancer cells and the antibody, where the detection of the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing a cancer, for treating cancer and for inhibiting expression of a CA gene in a cell. This sequence represents a human cancer-associated protein of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antidathmatic; antidrheumatic; antidathitic; antidation; antidation; antidammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; antipamation; caldiance cell disorder; autoimmune disorder; haemostatic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 OVSRGOKVISLIACLVDOSLRLDCRHENTSSSPIQYBFSLTRETKKHVLFGTVGVPEHTY
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTID-PADSY
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                                                                                                                                                                                                                                                                                                                                                       70.1%; Score 424; DB 9; Length 161; 73.9%; Pred. No. 1.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cancer associated protein sequence SEQ ID NO:1384.
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N-PSDB; AAC78148.
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                                                                                                                                                                                                                                                                                                                 Sequence 161 AA;
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon

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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the issues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antitheumatic; antiarthritic; antidiabetic; antisthyroid; antiallergic; antiarthritic; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; coorropic; vasotropic; antiporiatic and antiangiogenic. The polymucleotides and polypeptides can be used for preventing, treating or meliorating medical conditions and diagnosing pathological conditions. Polymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or imbibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, gradiovascular disorders, neurological disease and criminamation, cancers, cardiovascular disorders, neurological disease and consists and antagonists may be used in drug screens. AAC78449 to AAC78457 and AAB44440 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTID-PADSY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 TS-----YNONF-----KDEGTYTCALHHSGHSPPISSONVTVLRDKLVKCEGV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; colon cancer; colon cancer antigen; diagnosis; detection;
colorectal carcinoma; chromosome 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                               70.1%; Score 424; DB 3; Length 165; 73.9%; Pred. No. 1.3e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human colon cancer antigen protein SEQ ID NO:4614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG73850 standard; protein; 165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-2000; 2000WO-US026524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                            the present invention
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 165 AA;
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Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.

Claim 11; Page 6411-6412; 9803pp; English

Rosen CA;

Birse CE,

Ruben SM, Barash SC,

WPI; 2001-235357/24. N-PSDB; AAH33281

(HUMA-) HUMAN GENOME SCI INC.

99US-0157137P 99US-0163280P

29-SEP-1999; 03-NOV-1999;

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cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal sequences used in the exemplification of the present invention. N.B. C pages 666 to 682 and page 7053 of the sequence listing were missaing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 TS-----YNQNF-----KDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, mouse, rat, TEM; tumour endothelial marker; NEM; PEM; cytostatic, normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTID-PADSY
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                          Score 424; DB 4; Length 165;
Pred. No. 1.3e-37;
3; Mismatches 12; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Tumour Endothelial Marker polypeptide SEQ ID NO 220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       St Croix B, Kinzler KW, Vogelstein B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-2000; 2000US-022599P.
11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
                                                                                                                                                                                                                                                                                                                                                                                              70.1%;
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Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                           Sequence 165 AA;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
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                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                        Sequence 161 AA;
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06-DEC-1999
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                                      The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90735, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, necanglogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL921996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 TSYNONF-----KDEGTYTCALHHSGHSPPISSONVTVLRDKLVKCEGV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RS-RINFISKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGI 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; pc; pc; pan-endothelial marker; pc)ycyetic kidney disease; psoriasis; pan-endothelial marker; pc)ycyetic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; neoangiogenesis; namne response; cytostatic; antidiabetic, ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 422; DB 5; Length 161;
Pred. No. 2e-37;
3; Mismatches 11; Indels :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tumour endothelial marker TEM 13.
Claim 35; Page 194; 331pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU54451 standard; protein; 161 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                       69.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-2002; 2002WO-US008253
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nes 88; Conservative
                                                                                                                                                                                                                                                                                                                            (PEM) ABL91903-ABL91995
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N-PSDB; ABX72023.
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 161 AA;
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ABU5445.

Matches

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New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or

Disclosure; Page 206-207; 374pp; English.

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The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour andiogenesis, for for identifying candidate drugs for treating tumours. The present for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                       60 TSYNONF------KDEGTYTCALHHSGHSPPISSONVTVLRDKLVKCEGV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                            RS-RTNFTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Thy-1-Ig fusion, specifically claimed in Claim 8"
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                                                                                                                                                                                                                                                                                                                                                                                    74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angiogenesis; cancer; tumour; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting
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                                                                                                                                                                                                                                                                                                                                                    1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKRHVLFGTID-PADSY
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                         Score 422; DB 6; Length 161;
Pred. No. 2e-37;
3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Thy-1-human 1gG constant region fusion protein.
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/note= "Thy-1 signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY31789 standard; protein; 368 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-561618/47.
N-PSDB; AAX87980.
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which is claimed, comprising the human Thy-1 extracellular region (see AAY31787) and the constant region (hinge, CH2, CH3) of human 1gG1. A claimed method for inhibiting angiogenesis in a mammal comprises administering a compound that inhibits Thy-1 associated proliferation of an endothelial cell. The embethod is preferably the extracellular region of rat or human Thy-1. The method is preferably the extracellular region of rat or human Thy-1. The method is predict and associated with having a tumour (e.g. by reducing vascularisation), atherosclerosis or rheumatoid arthritis, the lesions of which may be associated with neovascularisation (all claimed). Another claimed method for inhibiting angiogenesis involves administering a Thy-1 antisense nucleic acid or a Thy-1 specific antibody linked to a cytotoxic agent. A method for promoting angiogenesis involves administering a compound that increases Thy-1 expression in an endothelial cell such as a chimeric protein comprising the Thy-1 extracellular fragment and the constant region of an immunoglobulin. (Updated on 17-OCT-2003 to standardise OS field) 

Sequence 368 AA;

ñ 75 RS-RTNFTSKYHMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEG 132 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTY 74 60 TSYNQNF------KDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEG 102 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTID-PADSY Gaps 18; Length 368; 11; Indels Score 419; DB 2; Pred. No. 1.2e-36; 2; Mismatches Query Match
Best Local Similarity 73.9%;
Matches 88; Conservative -12 셤 ò ò

ADW10183 standard; protein; 162 AA. 24-MAR-2005 ADW10183; RESULT 12 

셤

(first entry)

Human Thy-1 protein.

non-immunoglobulin binding polypeptide; selective binding; Thy-1.

ношо варіепв

US2004266993-A1.

30-DEC-2004

30-JUN-2003; 2003US-00611655

30-JUN-2003; 2003US-00611655.

(EVAN/) EVANS G A.

Evans GA;

WPI; 2005-047648/05.

New chimeric non-immunoglobulin binding polypeptide comprises immunoglobulin-like domain containing scaffold and exhibits selective binding activity, for producing non-immunoglobulin binding polypeptides with selective binding activity

Disclosure; SEQ ID NO 1; 45pp; English.

The invention relates to a novel chimeric non-immunoglobulin binding polypeptide. The polypeptide comprises an immunoglobulin-like domain containing scaffold with two or more solvent exposed loops containing a different complementarity-determining region (CDR) from a parent antibody inserted into each of the loops and exhibiting selective binding activity toward a ligand bound by the parent antibody. The invention further comprises: a chimeric Thyox binding polypeptide, comprising one or more

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-------KDEGTYTCALHHSGHSPPI-SSQNVTVLRDKLVKCEG 102
                                                                                                                                                                                                                                                                                                                            74
altered immunoglobulin-like domain loop regions of a ThyOx family polypeptide or at least one immunoglobulin-like domain containing scaffold derived from a ThyOx family polypeptide, and a heterologous binding polypeptide exhibiting selective binding activity toward a non-ThyOx ligand, and a nucleic acid encoding the non-immunoglobulin or ThyOx binding polypeptide above. The chimeric non-immunoglobulin binding polypeptides having selective binding activity toward a predetermined molecule. This sequence represents a human Thy-1 protein of the
                                                                                                                                                                                                                                                                                                                            15 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEESLTRETKKHVLFGTVGVPEHTY
                                                                                                                                                                                                                                                                                            1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTID-PADSY
                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                          Length 162;
                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                          Score 402.5; DB 5
Pred. No. 2.6e-35;
                                                                                                                                                                                                                 66.5%; Sco... 71.9%; Pred. No. c...
                                                                                                                                                                                                                                            Local Similario,
                                                                                                                                                                                                                                                                                                                                                                  60 TSYNONE
                                                                                                                                                                                           Sequence 162 AA;
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                                                                                                                                                           invention.
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RESULT 13 ADW10192

ADW10192 standard; protein; 176 AA. ADW10192;

(first entry) 24-MAR-2005 

Chimeric ThyOx carrier containing glucagon-like peptide 1.

non-immunoglobulin binding polypeptide; selective binding; ThyOx; glucagon-like peptide 1; GLP-1.

Synthetic. Chimeric.

US2004266993-A1.

30-DEC-2004

30-JUN-2003; 2003US-00611655.

(EVAN/) EVANS G A.

30-JUN-2003; 2003US-00611655.

Evans GA;

WPI; 2005-047648/05. N-PSDB; ADW10191 New chimeric non-immunoglobulin binding polypeptide comprises immunoglobulin-like domain containing scaffold and exhibits selective binding activity, for producing non-immunoglobulin binding polypeptides with selective binding activity.

Disclosure, SEQ ID NO 10; 45pp; English.

The invention relates to a novel chimeric non-immunoglobulin binding polypeptide. The polypeptide comprises an immunoglobulin-like domain a confaining scaffold with two or more solvent exposed loops containing a different complementarity-determining region (CDR) from a parent antibody inserted into each of the loops and exhibiting selective binding activity

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toward a ligand bound by the parent antibody. The invention further comprises: a chimeric Thyox binding polypeptide, comprising one or more altered immunoglobulin-like domain loop regions of a Thyox family polypeptide or at leads one inmunoglobulin-like domain containing scaffold derived from a Thyox family polypeptide, and a heterologous binding polypeptide exhibiting selective binding activity toward a non-Thyox ligand; and a nucleic acid encoding the non-immunoglobulin or Thyox binding polypeptide above. The chimeric non-immunoglobulin binding polypeptides having selective binding activity toward a non-bolypeptides having selective binding activity toward a predetermined molecule. This sequence represents a chimeric Thyox carrier containing glucagon-like peptide 1 of the invention.
                                                                                                                                                                                                                                                                                                                       49 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVDEHTYRS-RT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New chimeric non-immunoglobulin binding polypeptide comprises immunoglobulin-like domain containing scaffold and exhibits selective binding activity, for producing non-immunoglobulin binding polypeptides with selective binding activity.
                                                                                                                                                                                                                                                                                                  6 QKVTSLTACLVDQSLRLDCRHENTSSSNYMMHFSLTRETKKHVLFGTID-PADSYTSYNQ
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                65 NF-------KDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-immunoglobulin binding polypeptide; selective binding; ThyOx;
                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                       Length 176;
                                                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                     65.8%; Score 398; DB 9 72.2%; Pred. No. 9e-35;
                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erythropoietin protein, named SuperEpo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADW10190 standard; protein; 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2003; 2003US-00611655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                     Best Local Similarity 72.2
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erythropoietin; SuperEpo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-047648/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADW10189.
                                                                                                                                                                                                        Sequence 176 AA;
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polypeptide. The polypeptide comprises an immunoglobulin-like domain containing scaffold with two or more solvent exposed loops containing a different complementarity-determining region (CDR) from a parent antibody inserted into each of the loops and exhibiting selective binding activity toward a ligand bound by the parent antibody. The invention further comprises: a chimeric Thyox binding polypeptide, comprising one or more

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The invention relates to a novel chimeric non-immunoglobulin binding

Disclosure; SEQ ID NO 8; 45pp; English.

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                polypeptide or at least one immunoglobulin-like domain containing scaffold derived from a Thyox family polypeptide, and a heterologous binding polypeptide exhibiting selective binding activity toward a non-Thyox ligand; and a nucleic acid encoding the non-immunoglobulin or Thyox binding polypeptide above. The chimeric non-immunoglobulin binding polypeptide is useful for producing non-immunoglobulin binding polypeptides having selective binding activity toward a predetermined molecule. This sequence represents an erythropoietin protein, named SuperEpo, of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel chimeric non-immunoglobulin binding polypeptide. The polypeptide comprises an immunoglobulin-like domain containing scaffold with two or more solvent exposed loops containing a different complementarity-determining region (CDR) from a parent antibody inserted into each of the loops and exhibiting selective binding activity toward a ligand bound by the parent antibody. The invention further comprises a chimeric Thyox binding polypeptide, comprising one or more altered immunoglobulin-like domain loop regions of a Thyox family polypeptide or at least one immunoglobulin-like domain containing
                                                                                                                                                                                                                                                                                                                                                        207 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRS-RT 265
                                                                                                                                                                                                                                                                                                                              6 OXVISLIACIVDOSIRIDCRHENTSSSNYWMHFSLIRETKKHVLFGTID-PADSYTSYNQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New chimeric non-immunoglobulin binding polypeptide comprises immunoglobulin-like domain containing scaffold and exhibits selective binding activity, for producing non-immunoglobulin binding polypeptides with selective binding activity.
                                                                                                                                                                                                                                                                                            Gaps
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altered immunoglobulin-like domain loop regions of a ThyOx family polypeptide or at least one immunoglobulin-like domain containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-immunoglobulin binding polypeptide; selective binding; ThyOx;
                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                Score 398; DB 9; Length 334;
Pred. No. 2e-34;
3; Mismatches 11; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric ThyOx carrier containing erythropoietin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 6; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADW10188 standard; protein; 334 AA.
                                                                                                                                                                                                                                                    65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2003; 2003US-00611655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2003; 2003US-00611655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                          83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2005-047648/05.
                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADW10187
                                                                                                                                                                                                                Sequence 334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004266993-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erythropoietin.
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                                                                                                                                                                                                                                                      Query Match
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ADW10188
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CC scaffold derived from a ThyOx family polypeptide, and a heterologous binding polypeptide exhibiting selective binding activity toward a non-cryox ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx 1900 polypeptide above. The chimeric non-immunoglobulin binding collypeptide is useful for producing non-immunoglobulin binding collocule. This sequence represents a chimeric ThyOx carrier containing collocule. This sequence represents a chimeric ThyOx carrier containing collocule. This sequence sylvantion.

CC sythropoietin of the invention.

CC erythropoietin of the invention.

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Search completed: December 6, 2005, 10:36:49 Job time : 105.652 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

6, 2005, 10:32:12; Search time 18.5645 Seconds (without alignments) 575.296 Million cell updates/sec December Run on:

US-10-611-655-4 605 1 QVSRGQKVTSLTACLVDQSL......VLRDKLVKCEGVYYRYYFDY 111 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	tion	nypothetical prote	embrane gly	membrane gly	embrane gly	lycoprotein	y chain V r	_	Fab Je		y chain V r	chain V						_	_	chain	chain pr	chain	chain V	-	chain V	chain V	chain	chain V	chain V	y chain V r
	Description	hypothe	Thy-1 m	Thy-1 m	thy-1 m	Thy-1 g	Ig heavy	Ig heavy			Ig heavy	Ig heavy				Ig heavy		Ig heavy	Ig heavy		Ig heavy	Ig heavy			Ig heavy	Ig heavy		Ig heavy	Ig heavy	Ig heavy
SUMMARIES		30				75	48	45	51	75	94	50	36	46	64	54	52	09	32	63	24	125	05	24	18	38	55	33	34	62
ω	Ð	T47130	TDHOT	TDMS	TDRT	A48975	\$25048	S25045	S53751	825175	841394	D25150	\$25036	820646	PH1164	\$25054	825052	PH1160	\$25032	S264	PSOC	825025	PH1005	S25024	826318	\$25038	S25055	825033	825034	PH11
	80	2	Н	Н	-	7		7										7	7						~	~	~	7	~	N
	Query Match Length DB	1																				102								
de	Query Match	70.1	69.8	48.2	46.3	29.5	21.8	21.5	21.3	20.9	20.8	. 20.5	20.3	.20.2	20.5	20.5	20.2	20.0	19.8	19.8	19.8	19.7	19.7	19.7	19.6	19.5	19.5	19.3	19.3	19.2
	Score	424	422	291.5	280	176.5	132	130	129	126.5	126	124	123	122.5	122	122	122	121	120	120	120	119	119	119	118.5	118	118	117	117	116
	Result No.	-	7	e	4	S	9	7	80	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2

Thy...
Thy...
Thy...
Thy...
Thy...
Thy...
Thy...
Thy...
NyAlternate names: Thy.1 antigen
C;Species: Home sapiens (man)
C;Species: Home sapiens (miles: Home sapiens)
A;Title: The human Thy. Species: Home sapiens (miles: Home sapiens)
A;Title: The human Thy. I gene: structure and chromosomal location.
A;Reference number: A02106; MUID:86016759; PMID:2864690
A;Residues: 1-161 <SEK>
A;Cross-references: UNIPROT:P04216; UNIPARC:UP10000049811; GB:M11749; NID:g339682; PIDN
C;Genetics:
A;Gene: GDB:THY.
A;Cross-references: GDB:119614; OMIM:188230
A;Gene: GDB:11423
A;Introns: 13/1; 125/1

	Ig heavy chain V r	_	-		-	heavy	heavy	heavy		heavy	heavy	heavy	heavy	
S17613	825047	\$25051	B22769	S24287	826316	S20643	PH1004	S26320	817616	PH1561	PH0987	PL0089	PH1161	\$25030
2.0	4 (4	~	N	N	~	7	~	N	N	N	N	N	~	7
96	111	111	120	122	108	122	91	107	96	147	101	119	88	111
19.2	19.0	19.0	18.8	18.8	18.8	18.8	18.6	18.5	18.3	18.2	18.1	18.1	18.0	18.0
116	115	115	114	114	113.5	113.5	112.5	112	111	110	109.5	109.5	109	109
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 T47130 hypothetical protein DKFZp761B15121.1 - human C;Species: Homo sapiens (man) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004 C;Accession: T47130	R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, S. submitted to the Protein Sequence Database, March 2000 A;Reference number: 224374 A;Accession: T47130 A;Actession: T47130 A;Status: preliminary	A; Residues: 1-161 - AMA-A; Cross-references: UMI-PROT: P04216; UNIPARC: UPI0000136F1F; EMBL: AL161958 A; Experimental source: adult amygdala; clone DKFZp761B15121 . C; Genetics: DKFZp761B151211 A; Note: DKFZp761B151211 C; Superfamily: immunoglobulin V region; immunoglobulin homology	Owery Match 70.1%; Score 424; DB 2; Length 161; Best Local Similarity 73.9%; Pred. No. 2.1e-34; Matches 88; Conservative 3; Mismatches 12; Indels 16; Gaps	Qy 1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHPSLTRETKKHVLFGTID-PADSY 59	Qy 60 TSYNQNPKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGV 103

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A;Molecule type: protein
A;Residues: 20-130 <CAM>
A;Cross-references: UNIPARC:UPI0000173743
The Thy-1.2 sequence is shown.
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                                                           A; Map position: 9
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A/RCREGATION: A44278; MOID:85118360; PMID:2857501
A/RCREGATURE: UNIFOCT.PO1831; UNIFARC:UPI000002395E; GB:M10246; NID:G202032; PIDN:
R/ACCREGATURE: UNIFACT: GTGORVELA,
R/ACCREGATION: A2467; MOID:8605760; PMID:2866091
A/ACCREGATION: A2467; MOID:8219996; PMID:6177036
A/ACCREGATION: A2467; MOID:8219996; PMID:6177036
A/ACCREGATION: A2467; MOID:8219996; PMID:6177036
A/ACCREGATION: A2468
A/ACCREGATION: A2468; MOID:8219996; PMID:6177036
A/ACCREGATION: A2468
A/ACCREG
                                                                                                                                                                                                                                                                                                                                                                        3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thy-1 membrane glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jul-1982 Heaquence_revision 28-May-1986 #text_change 09-Jul-2004
C;Date: 06-Jul-1982 Heaquence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A94278; A24647; A34265; I59028; I55957; A02108
R;Seki, T.; Chang, H.C.; Moriuchi, T.; Denome, R.; Ploegh, H.; Silver, J.
Science 227, 649-651, 1985
A;Title: A hydrophobic transmembrane segment at the carboxyl terminus of Thy-1.
A;Reference number: A94278; MUID:85115360; PMID:2857501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KDEGTYTCALHHSGHSPPISSONVTVLRDKLVKCEGV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: glycoprotein; thymocyte; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-161/Product: Thy-1 membrane glycoprotein #status predicted <MAT>
F;20-141/Domain: extracellular #status predicted <EXI>
F;31-106/Domain: immunoglobulin homology <IMM>
F;31-106/Domain: transmembrane #status predicted <TWM>
F;142-161/Domain: transmembrane (ABN) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTID-PADSY
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                                                                                                                                                                                                                                                                                                  Query Match 69.8%; Score 422; DB 1; Length 161;
Best Local Similarity 73.3%; Pred. No. 3.3e-34;
Matches 88; Conservative 3; Mismatches 11; Indels
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A;Residues: 1-161 <SEK>
A;Cross-references: UNIPROT:P01830; UNIPARC:UPI0000136F21; GB:X02002; NID:957363; PIDN:C
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A;Residues: 1-70, 'Q', 72-161 <SE3>
A;Cross-references: UNIPARC:UPI0000170B3E; GB:X03152; NID:g57357; PIDN:CAA26931.1; PID:c
R;Moriuchi, T.; Silver, J.
R;Moriuchi, T.; Silver, J. 1984
ERBS Lett. 178, 105-107, 1984
A;Title: Rat Thy-1 antigen has a hydrophobic segment at the carboxyl terminus.
A;Reference number: A21652; MUID:85051865; PMID:6149956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Rat brain Thy-1 glycoprotein. The amino acid sequence, disulphide bonds and an A,Reference number: A90311; MUID:82068190; PMID:6118137
                                                                                                                                                                                                                                                                                                                                                                    Y----TSYNQ------NF--KDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGV 103
                                                                                                                                                                                                                                                                                                                                                                                                                       75 YRSRVTLSNQPYIKVLTLANFTTKDEGDYFCELQVSGANPMSSNKSISVXRDKLVKCGGI 134
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A; Molecule type: mRNA
A; Residues: 20-161 - (SB2)
A; Residues: 20-161 - (SB2)
A; Cross-references: UNIPARC: UPI0000170B3F
B; Seki, T.; Chang, H.C.; Moriuchi, T.; Denome, R.; Silver, J.
Réd. Proc. 44, 2865-2869, 1855
A; Title: Thy-1: a hydrophobic transmembrane segment at the carboxyl terminus.
A; Reference number: A25255; MUID: 86005549; PMID: 2864289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thy-1 membrane glycoprotein precursor - rat
N;Alternate names: thy-1 antigen
C;Species: Rattus norregiums (Norway rat)
C;Date: 29-Jun-1981 #sequence revision 08-Feb-1996 #text change 09-Jul-2004
C;Accession: B45909; A45909; A25255; A21652; A90311; A93296; A02107
R;Seki, T.; Moriuchi, T.; Chang, H.C.; Denome, R.; Silver, J.
Nature 313, 485-487, 1985
A;Title: Structural organization of the rat thy-1 gene.
A;Reference number: A45909; MUID:85111162; PMID:2857477
                                                                                                                                                                                                                                  1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMH-FSLTRETKKHVLFGTID-PADS
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A,Residues: 20-161 <MOR>
A,Residues: 20-161 <MOR>
A,Cross-references: UNIPARC:UPI0000170B3F, GB:X03150, GB:J00792; GB:X01445
R,Campbell, D.G.; Gggnon, J.; Reid, K.B.M.; Williams, A.F.
Biochem. J. 195, 15-30, 1981
A;Title: Rat brain Thy-1 glycoprotein. The amino acid sequence, disulphide
                                                                                                 Gaps
Query Match 48.2%; Score 291.5; DB 1; Length 162; Best Local Similarity 55.8%; Pred. No. 2e-21; Matches 67; Conservative 13; Mismatches 23; Indels 17;
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A;Status: preliminary
A;Status: useliminary
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule: 1-97, 'GS21', 102-111 <JAC>
A;Cross-references: UNIPARC:UPI00001160A0; EMBL;X67350; NID:g50900; PIDN:CAA47765.1; PI:
C;Superferantly: immunoglobulin v region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
P;11-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C;Accession: S25045
E;Jacob, J.; Kelsoe, G
submitted to: he EMBL Data Library, July 1992
A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophen A;Reference number: S25024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UP100011609D; EMBL:X67345; NID:950892; PIDN:CAA47760.1; PI:C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;II-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                       A;Cross-references: UNIPARC:UPI000011609E; EMBL:X67349; NID:g50898; PIDN:CAA47764.1; PIL
                                                                                                                                                                                                                   A;Accession: S25046
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-111 < GAC2>
A;Cross-references: UNIPARC:UPI000011609E; EMBL:X67346; NID:g50894; PIDN:CAA47761.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 SVKLSCKASGYTFTSYMMHWVKQRPGRGLEWICRIDPNSGGTKYNEKFKSKATLTVDKPS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTIDPADSYTSYNONFKDEGTYTCALHH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody Fab Jel 103 heavy chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 31-Dec-2004
C;Accession: S53751
R;Pokkuluri, P.R.; Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M. J. Mol. Biol. 243, 283-297, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 SLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH
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Pred. No. 5.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 33.3%; Pred. No. 5.6e-06;
Matches 31; Conservative 13; Mismatches 47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 SGHSPPISSQNVTVLRDKLVKCEGVYYRYFDY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STAYMQLSS--LTSEDSAVYYCARYYYAYYFDY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STACMQLSS--LTSEDSAVYYCARYYYAYYFDY 103
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A;Molecule type: nucleic acid
A;Residues: 1-111 <JAC>
                                                                      A,Status: preliminary
A,Molecule type: nucleic acid
A,Residues: 1-111 <JAC1>
           A;Reference number: S25024
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Best Local Similarity
Matches 31; Conserv
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A;Note: this sequence shows homologies with immunoglobulin domains
R;Moriuchi, T.; Chang, H.C.; Denome, R.; Silver, J.
Nature 301, 80-82, 1983
A;Title: Thy-1 cDNA sequence suggests a novel regulatory mechanism.
A;Reference number: A93296; MUID:83115223; PMID:6130472
A;Reference number: A93296; MUID:83115223; PMID:6130472
A;Residues: 1-122 <MO2>
A;Residues: 1-122 <MO2>
A;Residues: 1-122 <MO2>
A;Residues: 1-120 <MO3>
C;Reywords: glycoprotein is a major constituent of brain-cell membrane and is abunda C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: glycoprotein; membrane glycoprotein #status experimental <MAT>
F;31-106/Domain: signal sequence #status predicted <SIG>
F;0-130/Product: thy-1 membrane glycoprotein #status experimental <AMAT>
F;20/Nodified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment F;28-130,38-104/Disulfide bonds: #status experimental
F;42,93,117/Binding site: carbohydrate (Asn) (covalent) #status experimental
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C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence revision 01-Dec-1995 #text_change 20-Jun-2000
C;Accession: S25048; S25046; $\overline{8}$25049
R;Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny
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A;Note: sequence extracted from NCBI backbone (NCBIN:117489; NCBIP:117490)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thy-1 glycoprotein - chicken

C;Species: Gallus gallus (chicken)

C;Species: Gallus gallus (chicken)

C;Dacession: A48975

R;Dowsing, B.J.; Gooley, A.A.; Gunning, P.; Cunningham, A.; Jeffrey, P.L.

Brain Res. Mol. Brain Res. 14, 250-260, 1992

Brain Res. Mol. Brain Res. 14, 250-260, 1992

A;Reference number: A48975; MUID:93061794; PMID:1359371

A;Accession: A48975

A;Botus: preliminary

A;Botus: preliminary

A;Botus: preliminary

A;Botus: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVSRGQXVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTID-PADSY 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 46.3%; Score 280; DB 1; Length 161; l Similarity 50.4%; Pred. No. 2.7e-20; 60; Conservative 16; Mismatches 27; Indels
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Best Local Similarity
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Best Local Similarity 41.84
Matches 23; Conservative
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A;Molecule type: nucleic acid
A;Residues: 1-106 <JAC>
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                                                                                          Best Local Similarity
Matches 31; Conserv
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                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CjAccession: $25175
RiMonsstier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
RiMonsstier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
Rimonsstier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
A; Description: Structure and binding properties of monoclonal antibodies to core histone A; Reference number: $25174
A; Recession: $25175
A; Structure preliminary
A; Molecule type: mRNA
A; Residues: 1-120 < MON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC;UPI00001160C2; EMBL;X67620; NID:951856; PIDN:CAA47878.1; PID (5.Superfamily: immunoglobulin v region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology cimmunoglobulin homology < IMS F;15-98/Domain: immunoglobulin homology < IMN>
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: 541394
R; Margaritte, C.; Gilbert, D.; Brard, F.; Tron, F.
Submitted to the EMBL Data Library, January 1994
A; Description: Structural characterization of an (NZB X NZW)F1 mouse-derived IgM anti-L
A; Reference number: 541393
A; Accession: 541394
A; Accession: 541394
A; Accession: 541394
A; Residues: 1-120 <MAR>
A; Molecule type: mRNA
A; Residues: 1-120 <MARA
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology <IMM>
F; 15-98 / Domain: immunoglobulin homology <IMM>
                an antibody Fab fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
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Best Local Similarity 34.0%; Fred. No. 1.2e-vo;
Matches 33; Conservative 13; Mismatches 39; Indels
        fitle: Preparation, characterization and crystallization of Reference number: S53750; MUID:95018269; PMID:7523684
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A;Title: Preparation, characterization and crystallization A;Reference number: S53750; MUID:95018269; PMID:7523684 A;Accession: S53751 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-116 <POK> A;Residues: 1-116 <POK> A;Cross-references: UNIPROT:Q924P9; UNIPARC:UPI0000176DC3 C;Superfamily: immunoglobulin homology <IMM> CINDER C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 SGHSPPISSQNVTVLRDKLVKCEGVYY----RYYPDY 111
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ig heavy chain V region - mouse
C,Species Mns musculus (house mouse)
C,Species 19-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C,Accession: S25036
E,Jacob, J.; Kelseo, G.
Shutted to the EMBL Data Library, July 1992
A,Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny
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C;Daces 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Aug-1996
C;Dacession: D25150
R;Dildrop, R.; Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.
EMBO J. 3, 217-523, 1984
A;Title: A V region determinant (idiotope) expressed at high frequency in B
A;Reference number: A91000; MUID:84182519; PMID:6201362
                                                                                                                                                             19 SLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH
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   Length 120
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.5%; Score 124; DB 2; Length 69; 41.8%; Pred. No. 2e-05; ive 11; Mismatches 21; Indels
                                                             44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (AC38 260.2) - mouse (fragment)
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                                                                                                                                                                                                                                                    79 SGHSPPISSQNVTVLRDKLVKCEGVYY--RYYFDY 111
Score 126; DB 2;
Pred. No. 2.4e-05;
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                                                             16; Mismatches
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Search completed: December Job time: 19.5645 secs
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           Tay meay Cining the Fightin.

Tay intery Cining the Museulus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C; Accession: S2064
R; Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A; Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A; Reference number: S20639
A; Accession: S20646
A; Status: preliminary
A; Residues: 1-123 < LOS
A; Cross-references: UNIPARC: UPI0000116020; EMBL: X65001; NID: 952612; PIDN: CAA46134.1; PIL
C; Steywords: heteroterramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < LMM>
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C;Species: Mus musculus (house mouse)
C;Accession: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C;Accession: 25054
R;Jacob, J; Kelsoe, G
Bubmitted to the EMBL Data Library, July 1992
A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny
A;Reference number: S25024
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PH1164
R;Schittek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A;Title: Natural occurrence and origin of somatically mutated memory B cells in mice. A;Reference number: PH1105; MUID:9236455; PMID:1500855
A;Accession: PH1164
A;Residues: 1-98 c&CH>
A;Residues: 1-98 c&CH>
A;Cross-references: UNIPARC:UPI0000176BC6
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroctetramer: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.2%; Score 122.5; DB 2; Best Local Similarity 30.9%; Pred. No. 5.3e-05; Matches 30; Conservative 16; Mismatches 36;
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20.2%; Score 122; DB 2;
Best Local Similarity 41.8%; Pred. No. 4.6e-05;
Matches 23; Conservative 10; Mismatches 22.
Ig heavy chain V region - mouse
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A;Molecule type: nucleic acid
A;Residues: 1-111 <JAC>
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S25054
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PH1164
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A,Cross-references: UNIPARC:UP100001160A4; EMBL:X67358; NID:g50921; PIDN:CAA47771.1; PID C; Superfamily: immunoglobulin v region; immunoglobulin homology C; Superfamily: immunoglobulin homology cikeywords: heterotetramer; immunoglobulin homology cIMM>
C; Keywords: heterotetramer; immunoglobulin homology cIMM>
Query Match

Query Match

Query Match

Best Local Similarity 32.3%; Pred. No. 5.3e-05;
Matches 30; Conservative 13; Mismatches 48; Indels 2; Gaps 1;
Matches 30; Conservative 13; Mismatches 48; Indels 2; Gaps 1;

Qy 19 SIRLDCRHENTSSSNYWMHFSLTRETKGHVLPGTIDPADSYTSYNQNFKDEGTYTCALHH 78

13 SYKLSCKASGYTFTSYWMHWYKQRPGGIEWIGRIDPNSGGTKYNBKFKSKATLTVDKPS 72

Qy 79 SGHSPPISSQNYTVLRDKLVKCGRYRYGSYFDY 101

Qp 73 STAXMOLSS--LTSEDSANYYCARRYYGSYFDY 103

Db 73 STAXMOLSS--LTSEDSANYYCARRYYGSYFDY 103
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6, 2005, 10:42:44

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Sequence Seq

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Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database :

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QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHPSLTRBTKKHVLFGTIDPADSYT
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; Sequence 20, Application US/1032281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer; TITLE OF INVENTION: Novel Compositions and Methods in Cancer; TITLE OF INVENTION: NOVEL COMPOSITION OF CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: ThyOx non-immunoglobulin binding polypeptide US-10-611-655-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SYNQNPKDEGTYTCALHHSGHSPISSQNVTVLRDKLVKCEGVYXRXYFDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10611655
Sequence 4, Application US/10611655
Publication No. US2004026693A1
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
FILE REPERENCE: 66663-026
CURRENT APPLICATION NUMBER: US/10/611,655
CURRENT FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 605; DB 5; Length 1
Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 111; Conservative 0; Mismatches 0; Indels
US-10-096-246-12

US-09-940-727B-118

US-09-940-727B-118

US-10-879-994-82

US-10-899-087A-18

US-10-689-006-18

US-10-610-452-14

US-10-10-452-14

US-10-134-93-99

US-10-012-482-1

US-10-012-482-1

US-10-013-482-1

US-10-013-482-1

US-10-013-482-1

US-10-013-482-1

US-10-013-613-857-2

US-10-803-623-226

US-10-803-623-226

US-10-803-633-226

US-10-937-046-9
                        10-727B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
    TYPE: PRT
ORGANISM: Homo sapiens
    RESULT 2
US-10-322-281-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 111
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Sequence 303, App
Sequence 303, App
Sequence 49897, A
Sequence 30, Appl
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Sequence 4624, Ap
Sequence 220, App
Sequence 220, App
Sequence 1, Appli
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Sequence 1, Appli
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Sequence 66, Appl
Sequence 449, App
Sequence 1149, Ap
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1, Appli
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8, Appli
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Sequence 4, Appli
Sequence 2, Appli
Sequence 23, Appli
Sequence 14, Appl
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                                                                                                                                                                   6, 2005, 10:32:17; Search time 87.0209 Seconds (without alignments) 532.965 Million cell updates/sec
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Sequence 8, App
Sequence 17, App
Sequence 303, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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605
1 QVSRGQKYTSLTACLVDQSL......VLRDKLVKCEGVYYRYYPDY 111
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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                               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-165-603-32

US-10-287-436A-449

US-10-287-436A-1149

US-09-925-301-1384

US-09-91-15-220

US-10-106-698-4624

US-09-918-715-220

US-10-474-794-220

US-10-611-65-10

US-10-611-65-10

US-10-611-65-8

US-10-11-65-8

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US-10-450-763-49895
US-10-816-938-23
US-10-683-547-14
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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264.5 186.5 162 129.5 127.5

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Gaps

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Length 111;

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QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKGVVLFGTVGVPEHTY 74
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                                                                      15 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTY 74
                                                                                                                                                              60 TS-----YNQNF-----KDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGV 103
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                                                                                                                                                                                                                                                                                                               RESULT 5
US-10-287-436A-449
i Sequence 449, Application US/10287436A
i Publication No. US20050202421A1
i GENERAL INFORMATION:
i APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
i TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: RHEUMATOID ARTHRITIS
i FILE REFERENCE: 10872-514696
i CURRENT APPLICATION NUMBER: US/10/287,436A
i CURRENT FILING DATE: 2002-10-31
i PRIOR PILING DATE: 2001-10-31
i NUMBER OF SEQ ID NOS: 1446
i SOFTWARE: PastSEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.1%; Score 424; DB 5; Length 161; 73.9%; Pred. No. 3.7e-37; tive 3; Mismatches 12; Indels
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Publication No. US20050202421A1

GENERAL INFORMATION:
APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
1TILE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
1TILE OF INVENTION: RHEUMATOID ARTHRITIS
FILE REFERENCE: 10872.514696
CURRENT APPLICATION NUMBER: US/10/287,436A
CURRENT FILING DATE: 2002-10-31
PRIOR PELING DATE: 2001-10-31
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1149
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Best Local Similarity 73.94
Matches 88; Conservative
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Matches 88; Conservative
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ORGANISM: Homo sapiens
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US-10-287-436A-449
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                                                                                                                                                                                             1 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSNYWMHFSLTRETKKHVLFGTIDPADSY- 59
                                                                                                                                                                                                                              15 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHYS 74
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Publication No. US20040146516A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Utah Ventures
TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
FILE REPERENCE: 27110-715
CURRENT APPLICATION NUMBER: US/10/794,899
CURRENT FILING DATE: 2004-03-05
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
SEQ ID NO 66
LENGTH: 161
                                                                                                                                                                                                                                                                                                                          60 ----TSYNQNF-----KDEGTYTCALHHSGHSPPISSONVTVLRDKLVKCEGV 103
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                                                                                                                                   14;
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                                                         Query Match 70.2%; Score 425; DB 4; Length 159; Best Local Similarity 73.5%; Pred. No. 2.8e-37; Matches 86; Conservative 4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32, Application US/10165603
| Publication No. US20030021792A1
| GENERAL INFORMATION:
| APPLICANT: Roben, Paul W. |
| APPLICANT: Stevens, Anthony C. |
| TITLE OF INVENTION: PROTEINS |
| FILE REFERENCE: TYECH.001A |
| CURRENT APPLICATION NUMBER: US/10/165,603 |
| CURRENT PILING DATE: 2002-06-07 |
| PRIOR APPLICATION NUMBER: 60/297,021 |
| PRIOR PILING DATE: 2001-06-08 |
| PRIOR PILING DATE: 2001-06-08 |
| PRIOR PILING DATE: 2001-06-08 |
| PRIOR PILING DATE: 2001-06-12 |
| NUMBER OF SEQ ID NOS: 33 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 32 |
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Best Local Similarity 73.9
Matches 88; Conservative
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ORGANISM: Homo sapiens
US-10-794-899-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapien
US-10-322-281-20
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Best Local S:
Matches 88;
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60 TSYNONF-----KDEGTYTCALHHSGHSPPISSONVTVLRDKLVKCEGV 103
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15 QVSRĞQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTY
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                                                                                                                                                     US-09-918-715-220

### Sequence 220, Application US/09918715
### Sequence 220, Application US/09918715
### Sequence 220, Application US/09918715
### Septication No. US20030017157A1
### Septication No. US20030017157A1
### APPLICANT: Bert Vogelstein
### APPLICANT: Renneth Kinaler
### TILLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
### TILLE OF INVENTION NUMBER: 60/999
### CURRENT APPLICATION NUMBER: 60/222,599
### PRIOR PILING DATE: 2000-08-01
### PRIOR PILING DATE: 2000-08-11
### PRIOR PILING DATE: 2000-08-11
### PRIOR PILING DATE: 2000-04-11
#### PRIOR PILING DATE: PIL
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US-10-474-794-220
i Sequence 220, Application US/10474794
j Publication No. US20040213793A1
j GENERAL INFORMATION:
d APPLICANT: Garson-Walter, Eleanor
j APPLICANT: St. Carson-Walter, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Winzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT FILING DATE: 2003-10-14
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOOTWARE: EsetSEQ for Windows Version 4.0
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Best Local Similarity 73.3%; Pred. No. 6e-37;
Matches 88; Conservative 3; Mismatches 11; Indels
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Best Local Similarity
Matches 88; Conserv
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LENGTH: 161
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Sequence 4624, Application US/10106698

Publication No. US20030109690A1

GENERAL INFORMATION:
APPLICANT: Ruben et al.
CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT APPLICATION NUMBER: US 60/157,137

PRIOR PRILING DATE: 1999-11-03

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564
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                                                75 RSRTNPTSKYNMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRDKLVKCEGI 133
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| Sequence 1384, Application US/09925301
| Patent No. US20020053308A1
| Patent No. US20020053308A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REPERENCE: PA106
| CURRENT APPLICATION NUMBER: US/09/925,301
| CURRENT PILING DATE: 2001-08-10
| PRIOR PILING DATE: 2000-03-08
| PRIOR PILING DATE: 1999-03-12
| PRIOR PILING DATE: 1999-03-12
| NUMBER: OF SEQ ID NOS: 1694
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 1384
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SEQ ID NO 4624
LENGTH: 165
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Matches 88; Conservative
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49 QKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRS-RT 107
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                                                                           KDEGTYTCALHHSGHSPPI-SSQNVTVLRDKLVKCEG 102
                                                                                                                               75 RS-RINFISKYHMKVLYLSAFTSKDBGTYTCALHHSGHSPPILSSQNVTVLRDKLVKCEG 133
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      15 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEESLTRETKKHVLFGTVGVPEHTY 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels 18;
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; Sequence 6, Application US. US204026693A1
; Publication No. US204026693A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
; TITLE OF INVENTION: NUMBER: US/10/611,655
; CURRENT APPLICATION NUMBER: US/10/611,655
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 65.8%; Score 398; DB 5; Length 176; Best Local Similarity 72.2%; Pred. No. 2.5e-34; Matches 83; Conservative 3; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/10611655
Publication No. US20040266993A1
GENERAL INFORMATION:
APPLICANT: EVANS, Glen A.
TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
FILE REPRENCE: 66663-026
CURRENT APPLICATION NUMBER: US/10/611,655
CURRENT PILING DATE: 2003-06-30
NUMBER OP SEQ ID NOS: 13
SOFTWARE: FARESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 72.23
Matches 83; Conservative
                                                                    60 TSYNONF-
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TYPE: PRT
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US-10-611-655-6
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15 QVSRGQKVTSLTACLVDQSLRLDCRHENTSSSPIQYEFSLTRETKKHVLFGTVGVPEHTY 74
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                                                                                                                                                                                                                                                                                                              Geguence 220, Application US/10979159;
Publication No. US20050142138A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107,00134
CURRENT APPLICATION NUMBER: US/10/979,159
CURRENT APPLICATION NUMBER: US/09/918,715
PRIOR APPLICATION NUMBER: G/222,599
PRIOR PILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: G/222,599
PRIOR PLING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: G/224,360
PRIOR PLING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: G/224,360
PRIOR PLING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: G/224,360
PRIOR APPLICATION NUMBER: G/224,360
PRIOR PLING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: G/282,850
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Publication No. US20040266993A1
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
FILE REFERENCE: 6663-026
CURRENT APPLICATION NUMBER: US/10/611,655
CURRENT PAPPLICATION NUMBER: US/10/611,655
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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